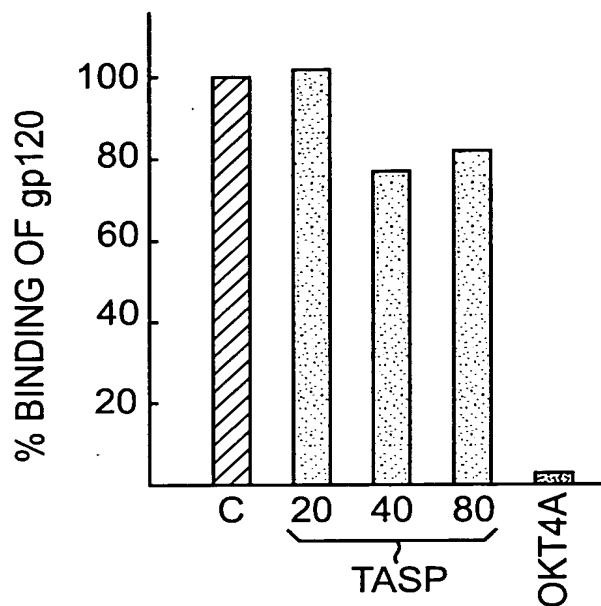




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A. BINDING OF gp120



B. BINDING OF HIV-1

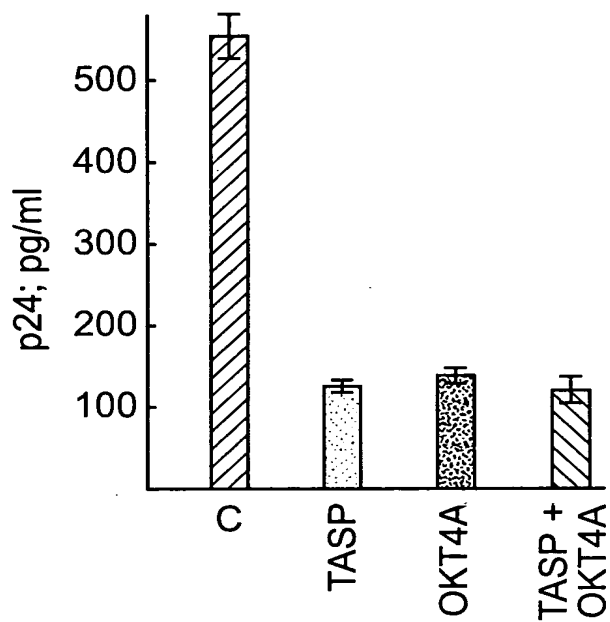


FIG. 1

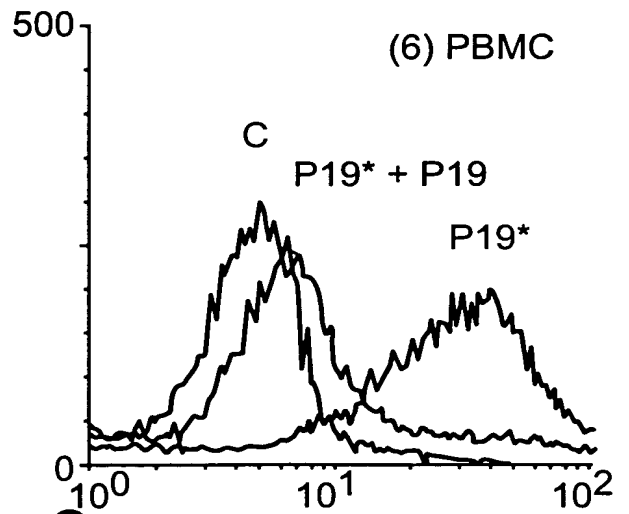
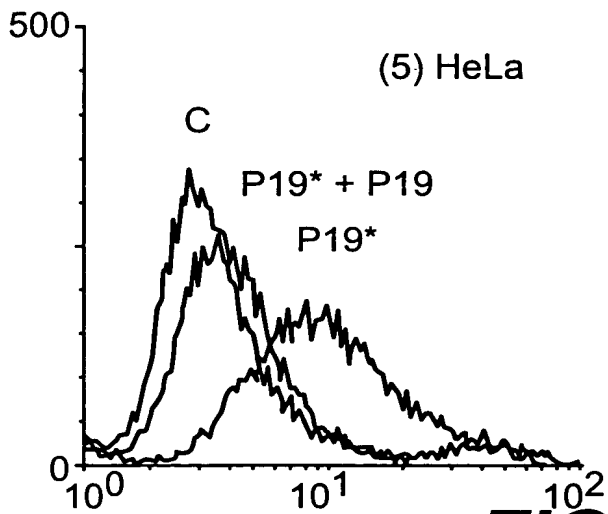
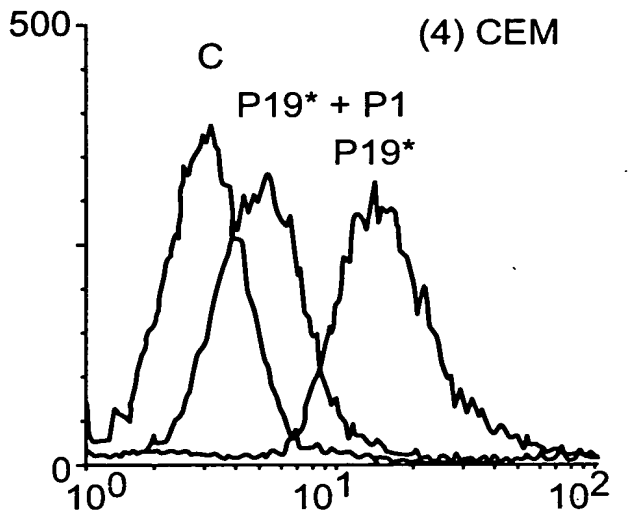
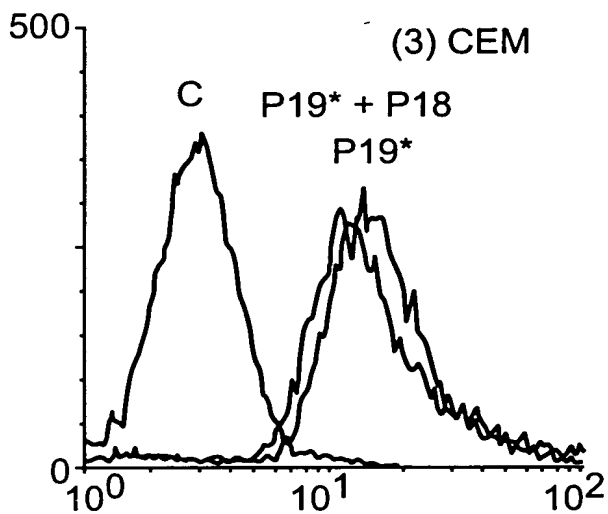
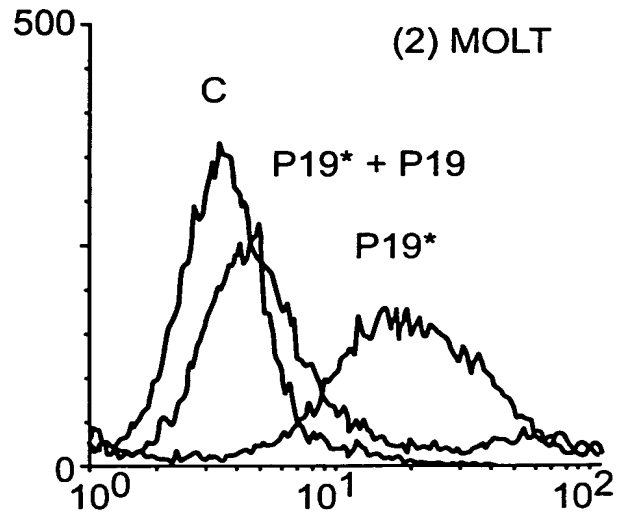
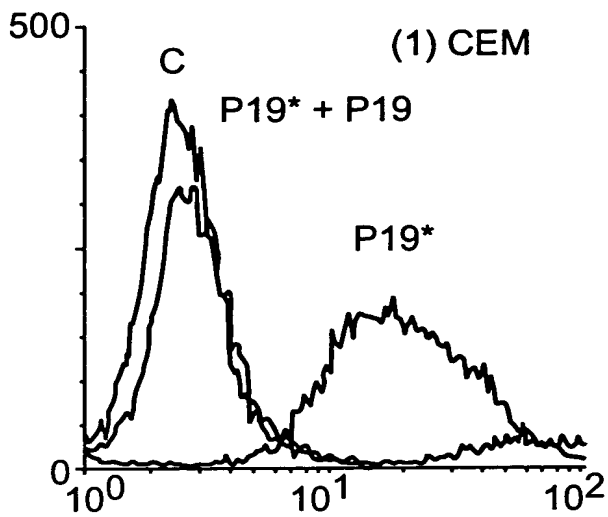


FIG. 2

SELECTED PREFERENCES:

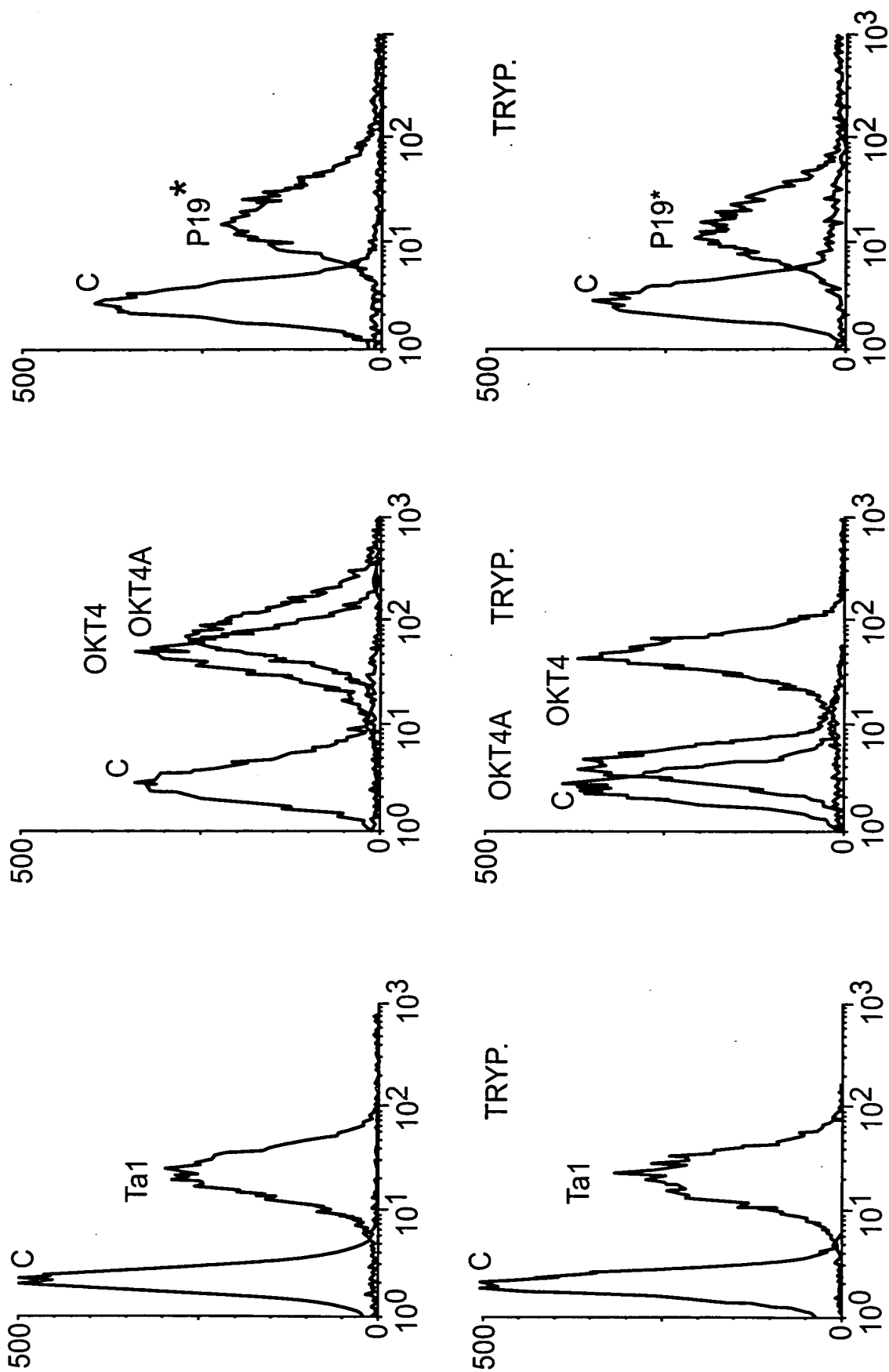


FIG. 3A



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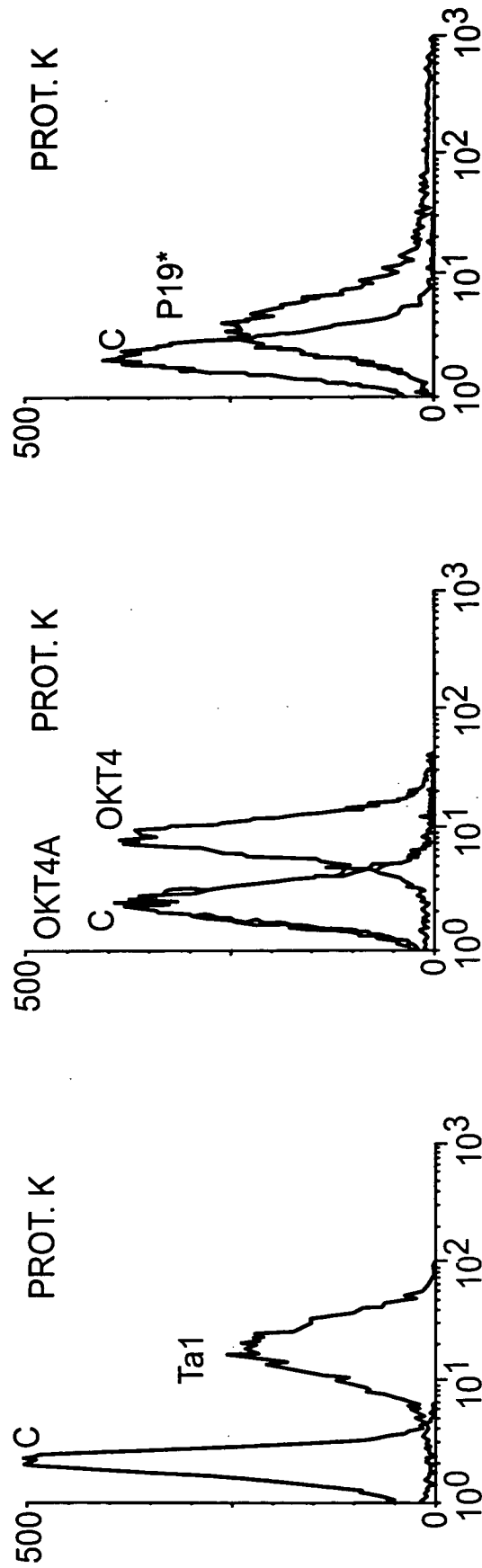


FIG. 3B



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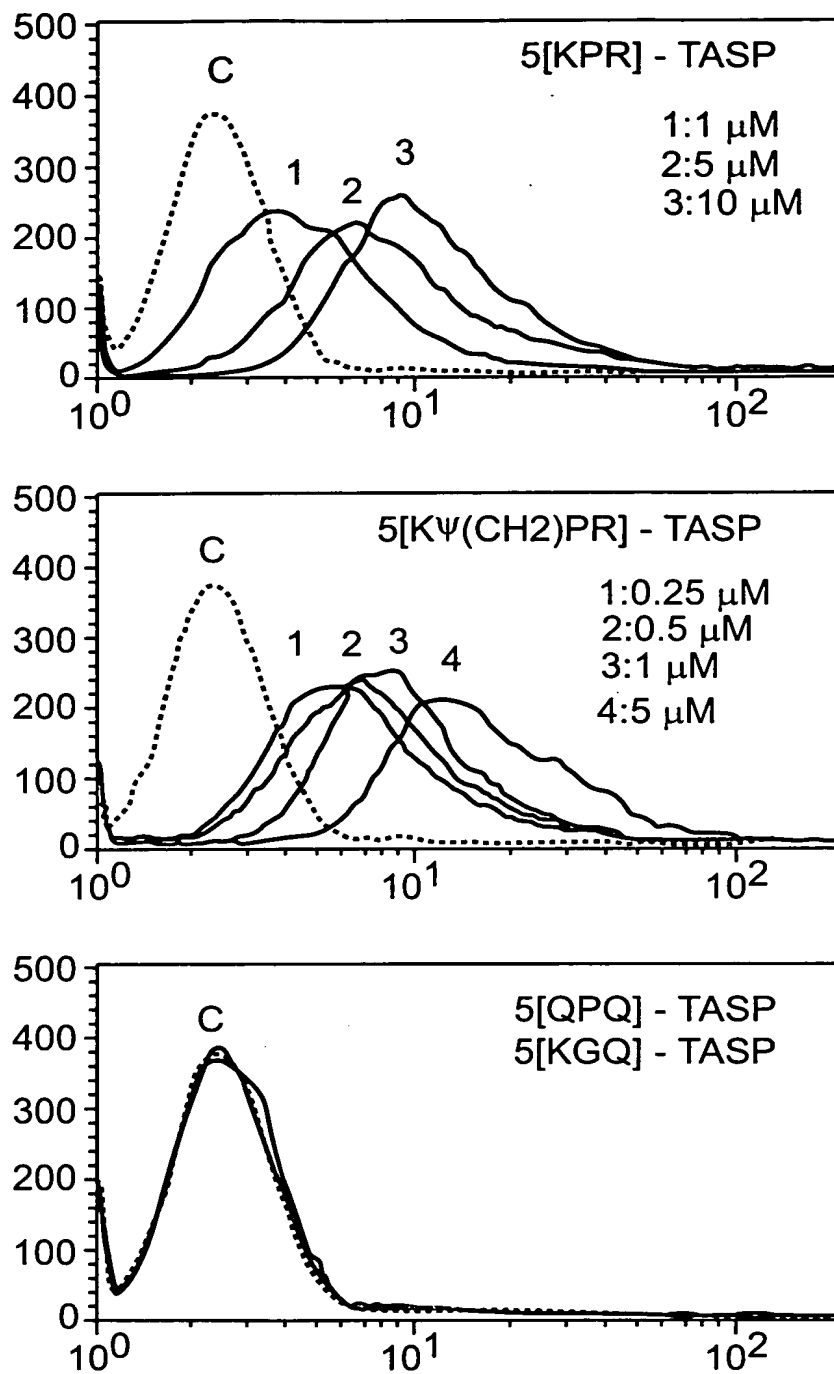


FIG. 4



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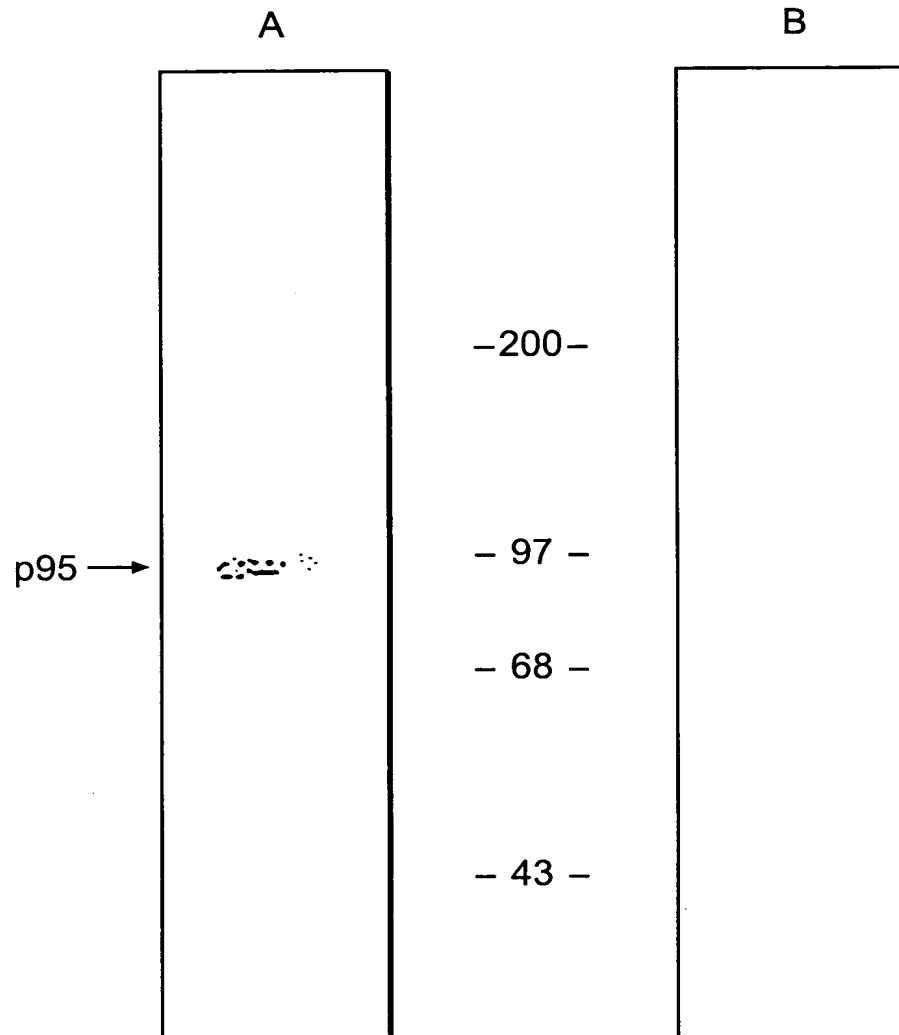


FIG. 5



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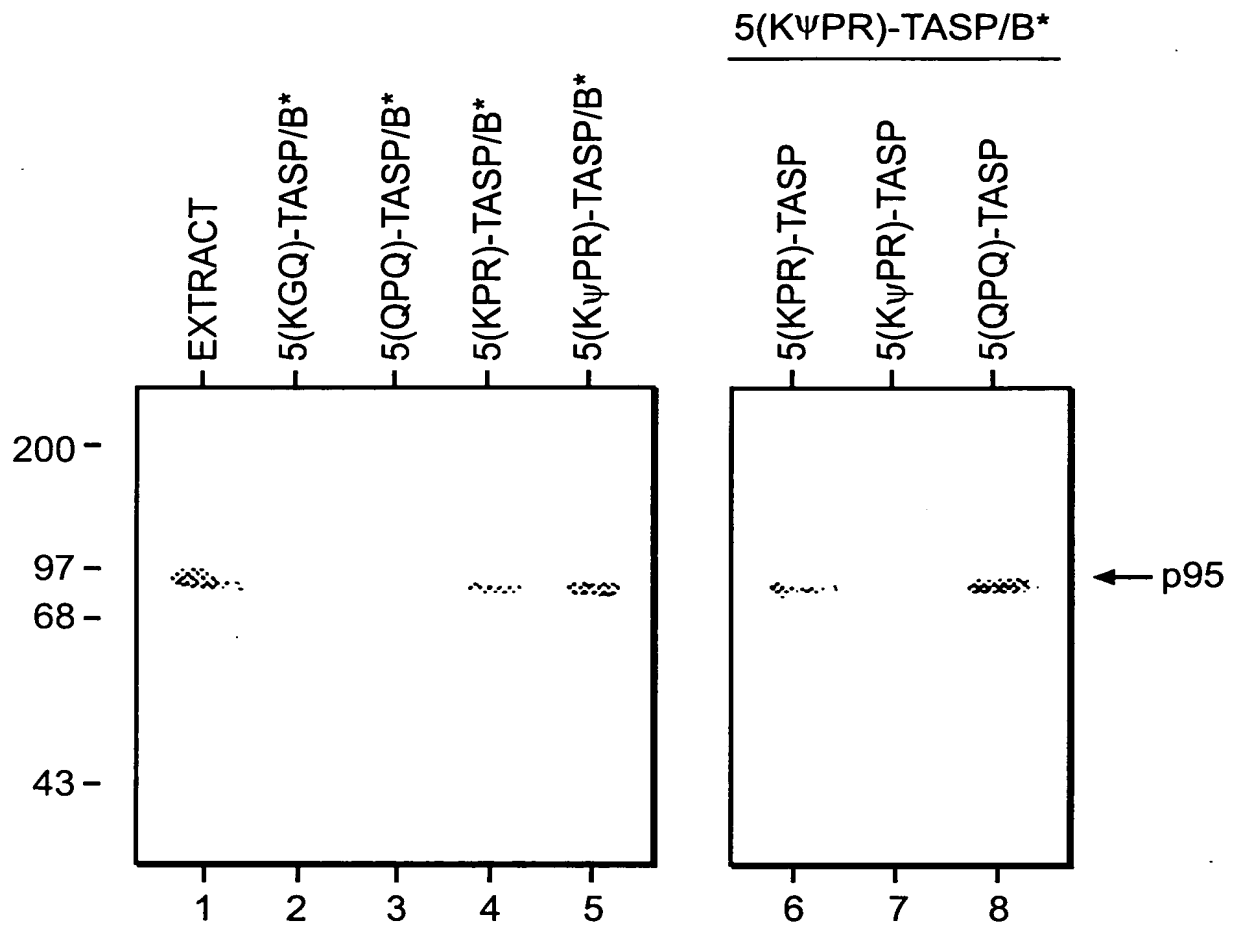


FIG. 6



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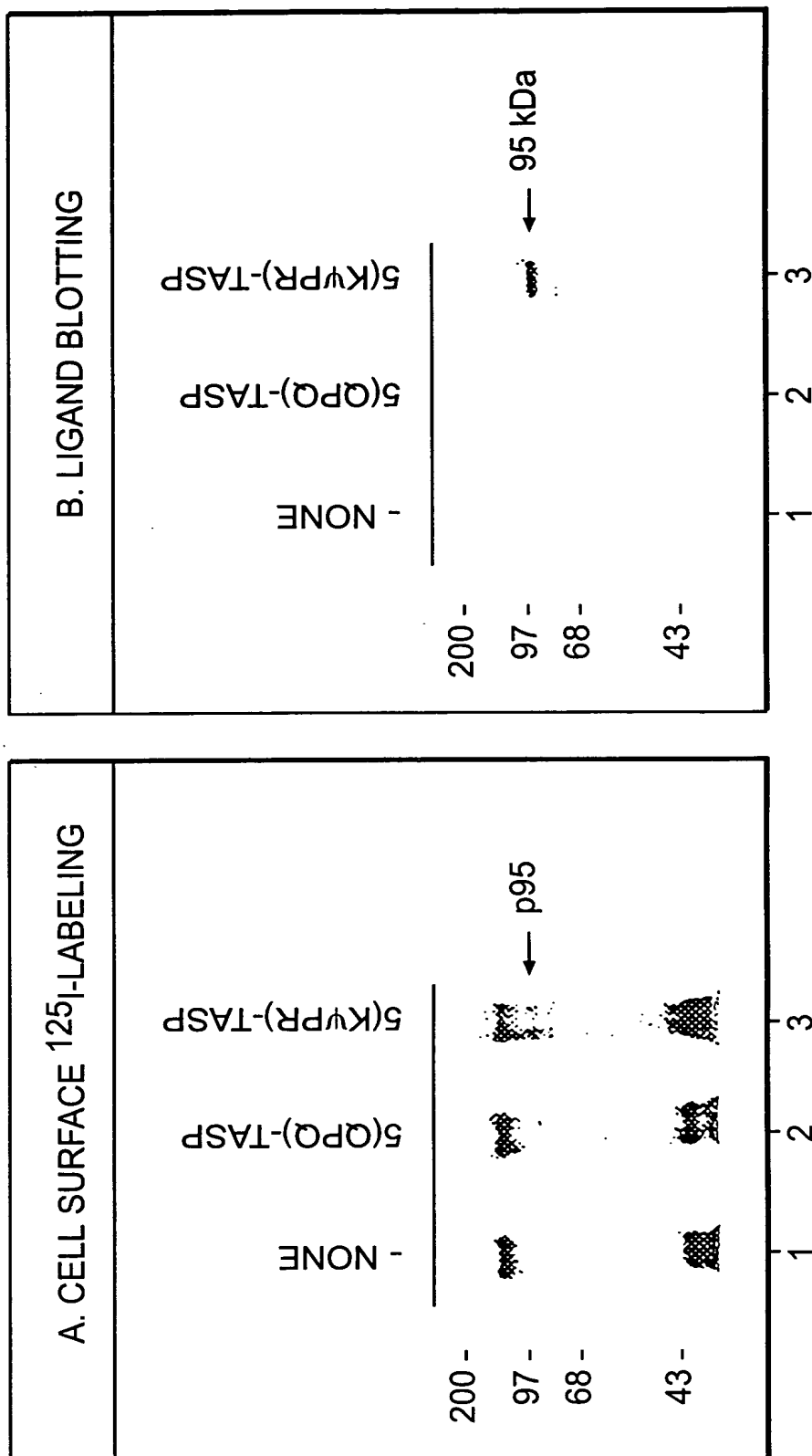


FIG. 7



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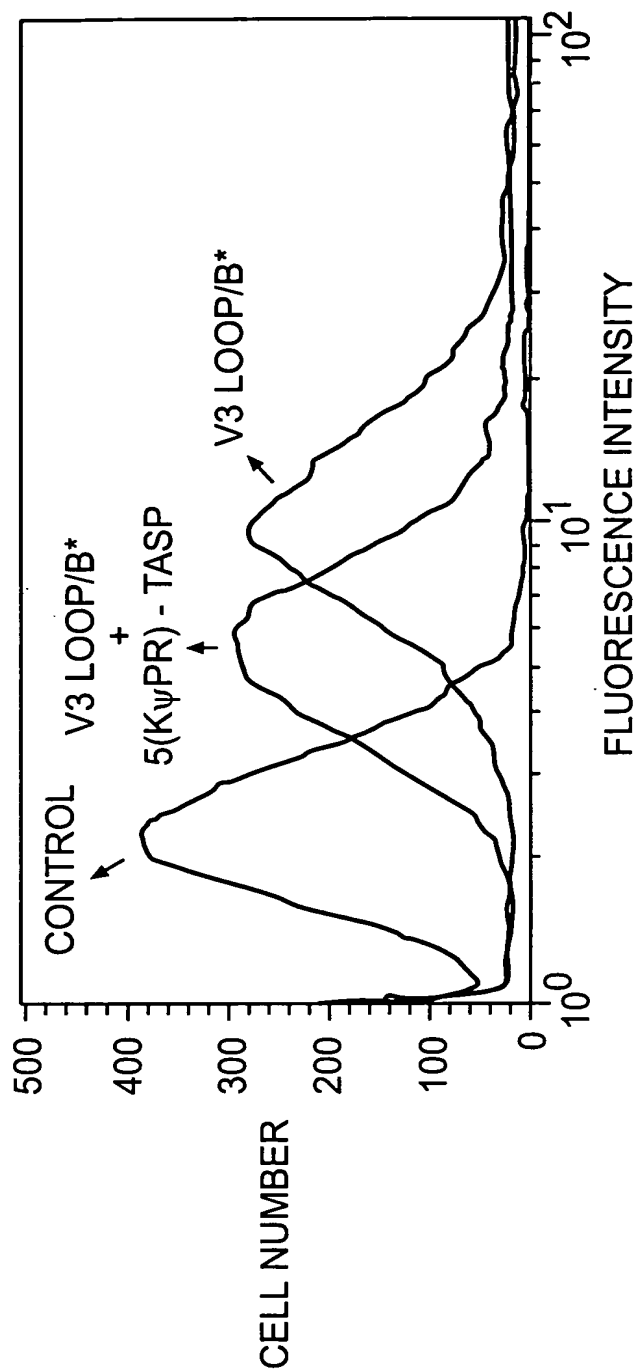


FIG. 8A



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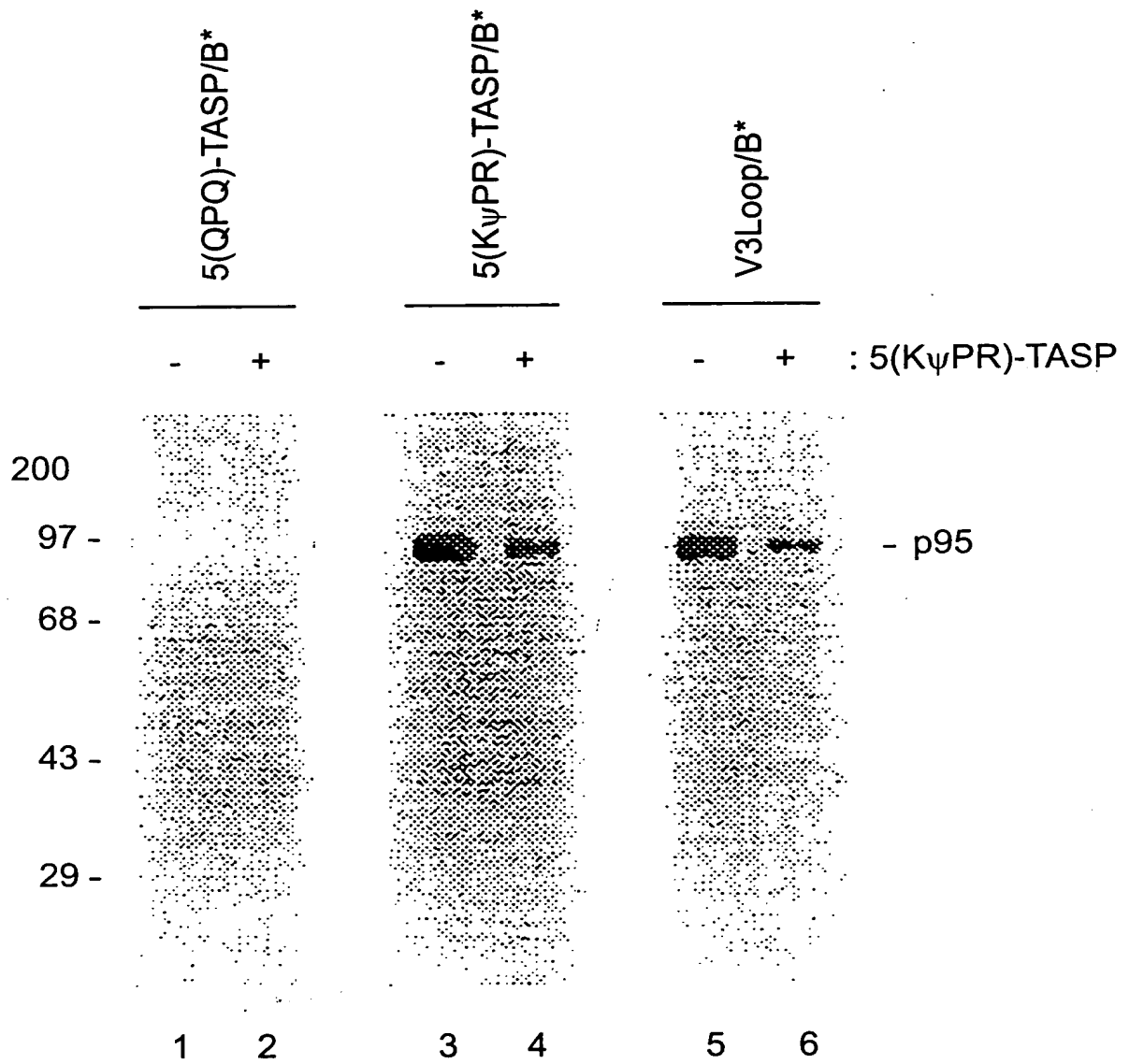


FIG. 8B



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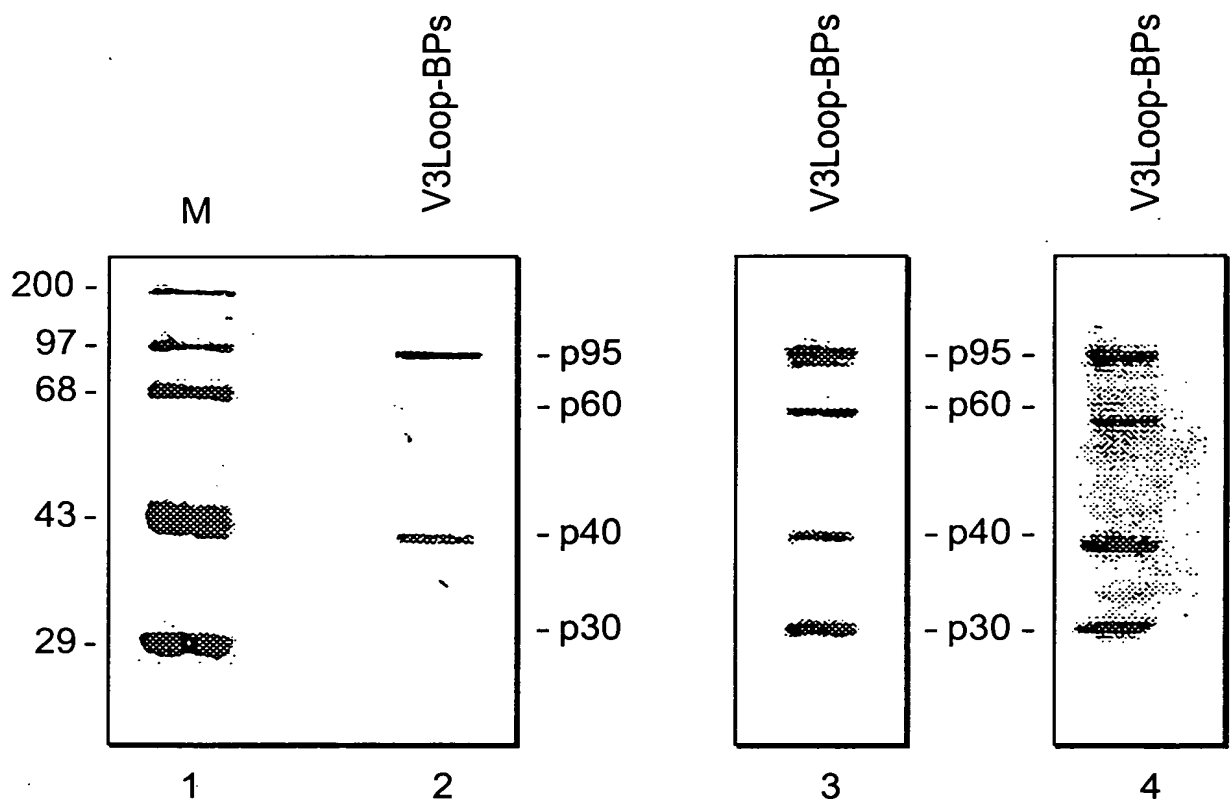


FIG. 9



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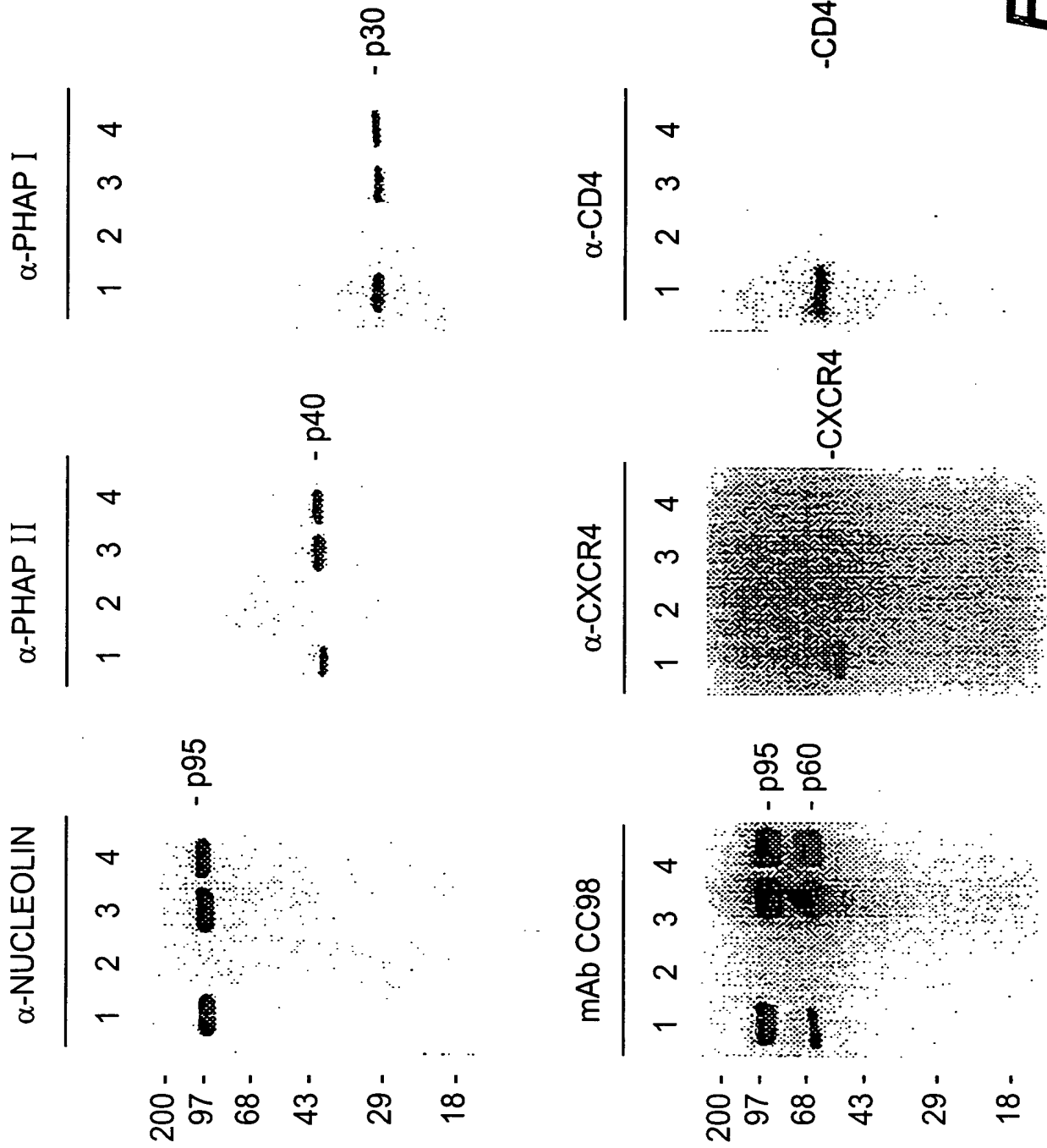


FIG. 10

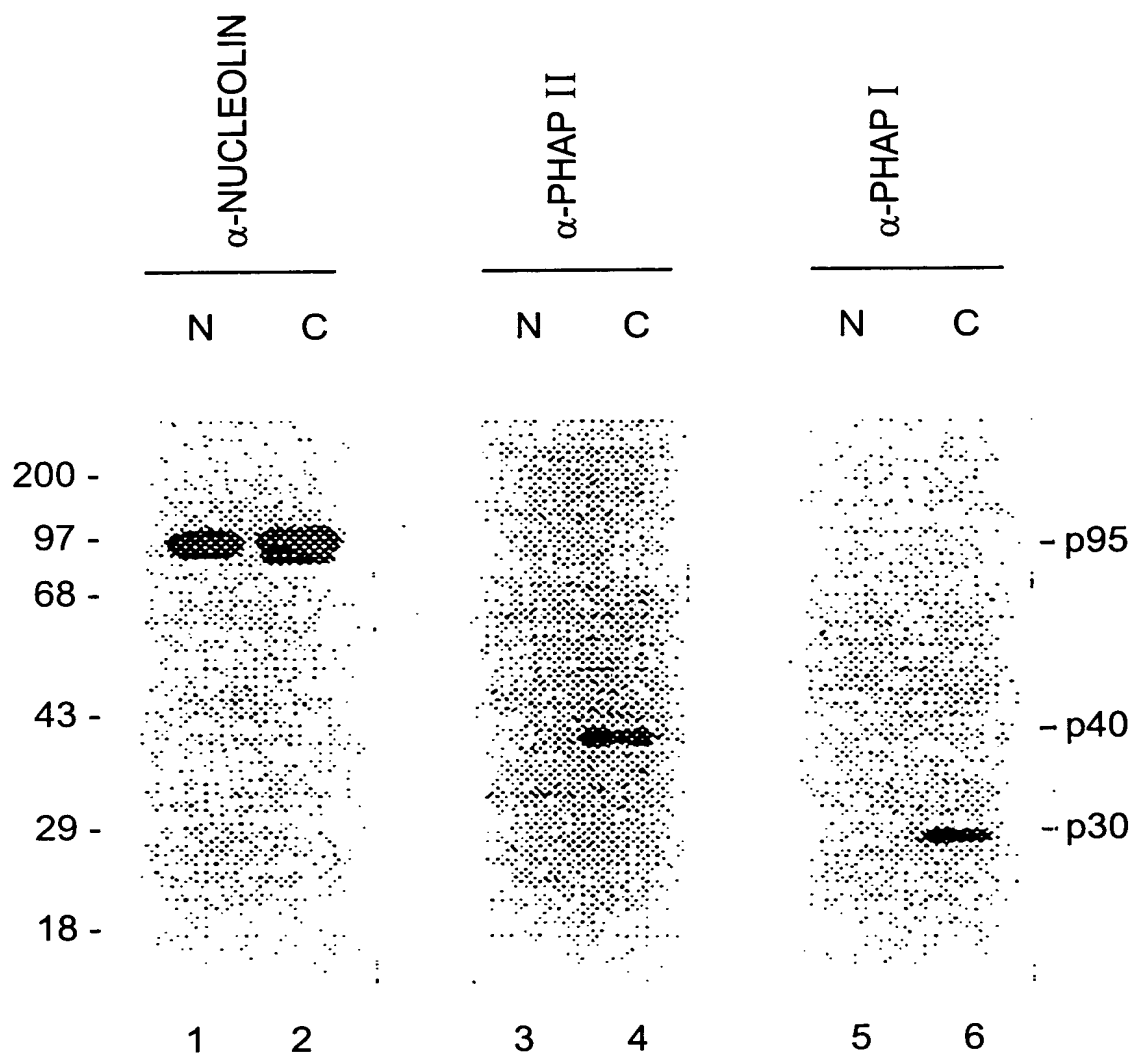


FIG. 11



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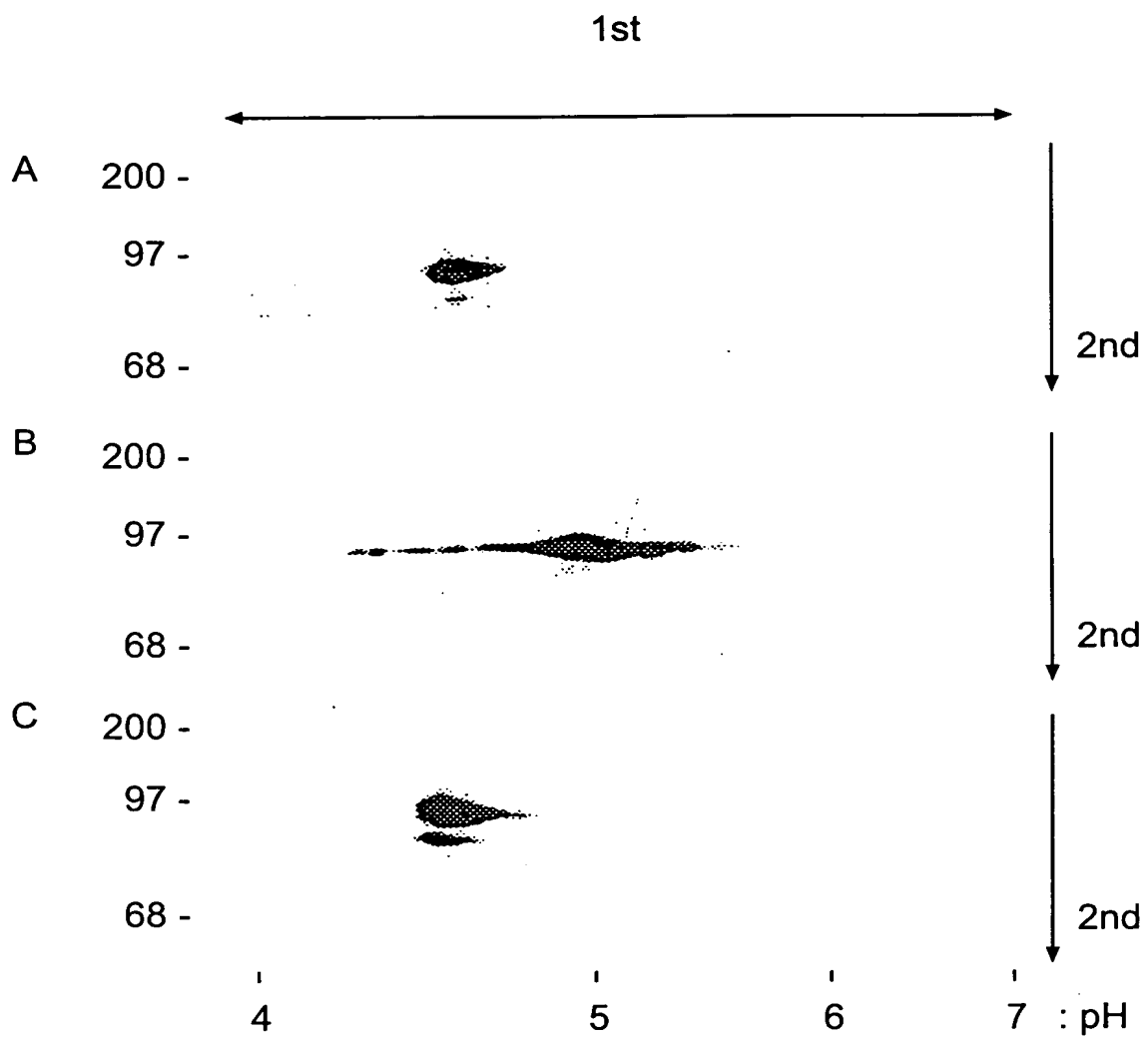


FIG. 12



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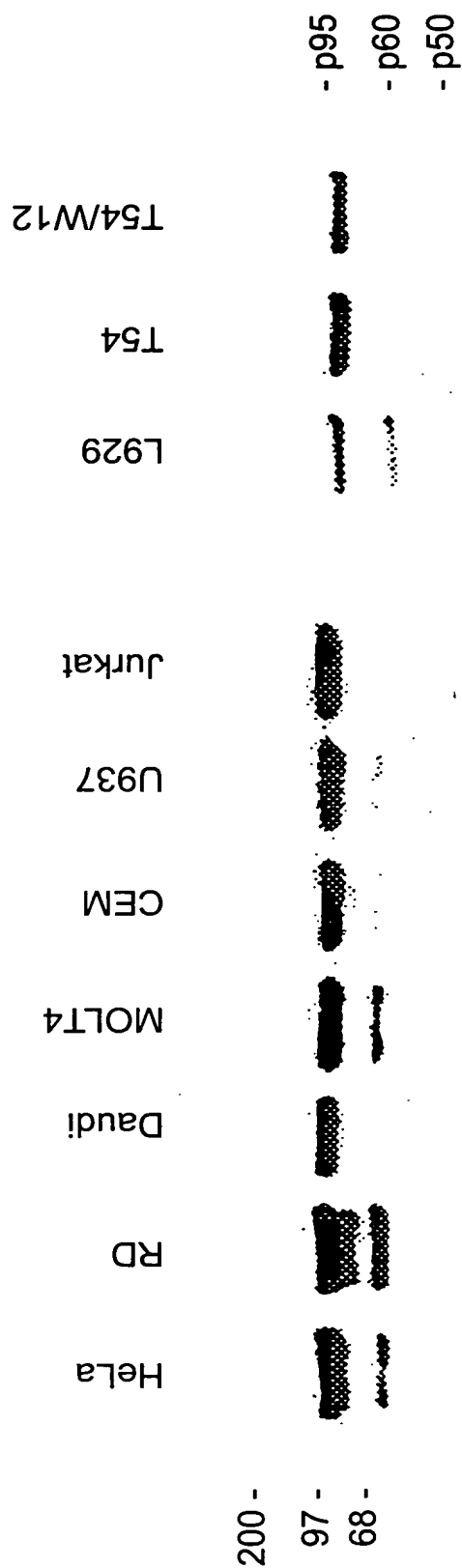


FIG. 13A



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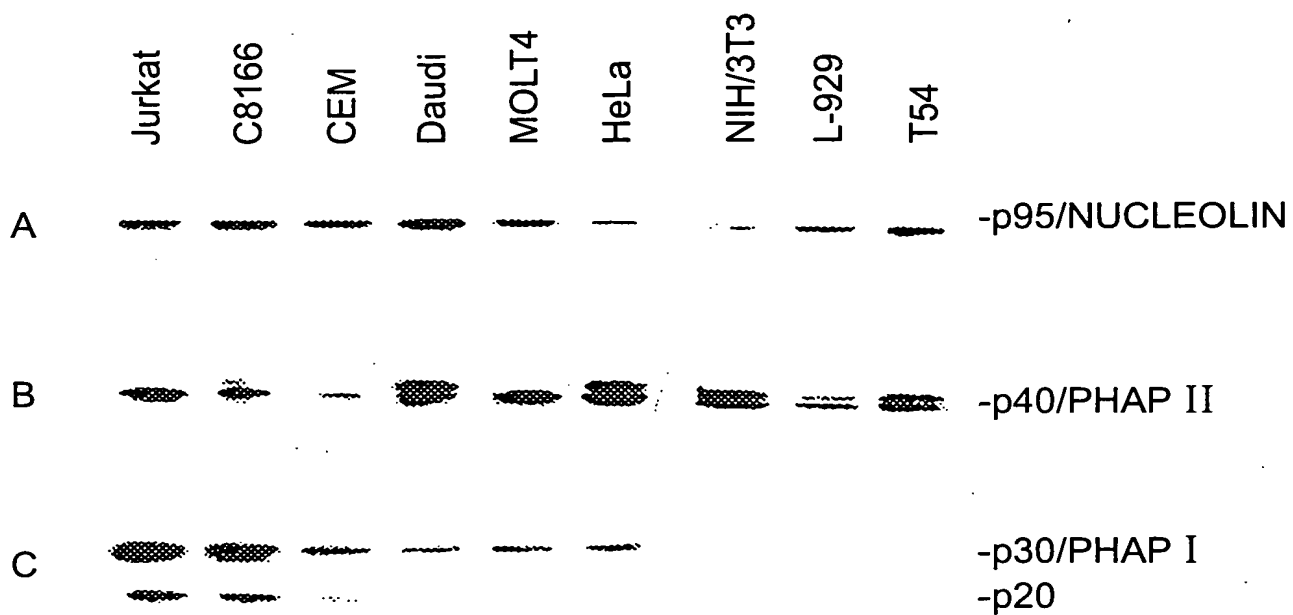


FIG. 13B



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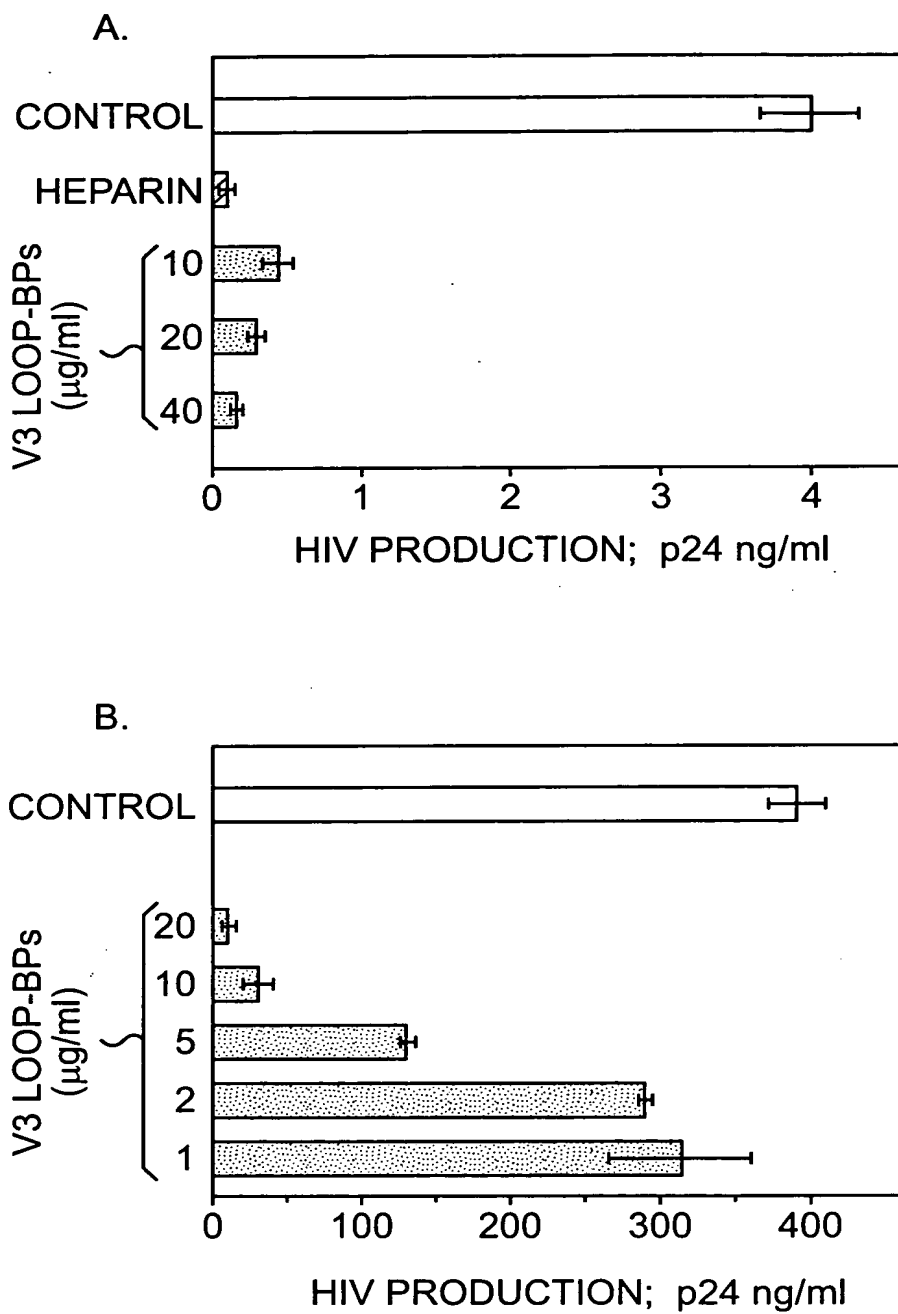
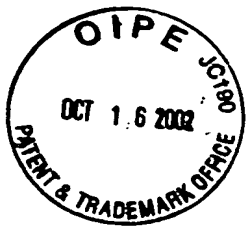


FIG. 14



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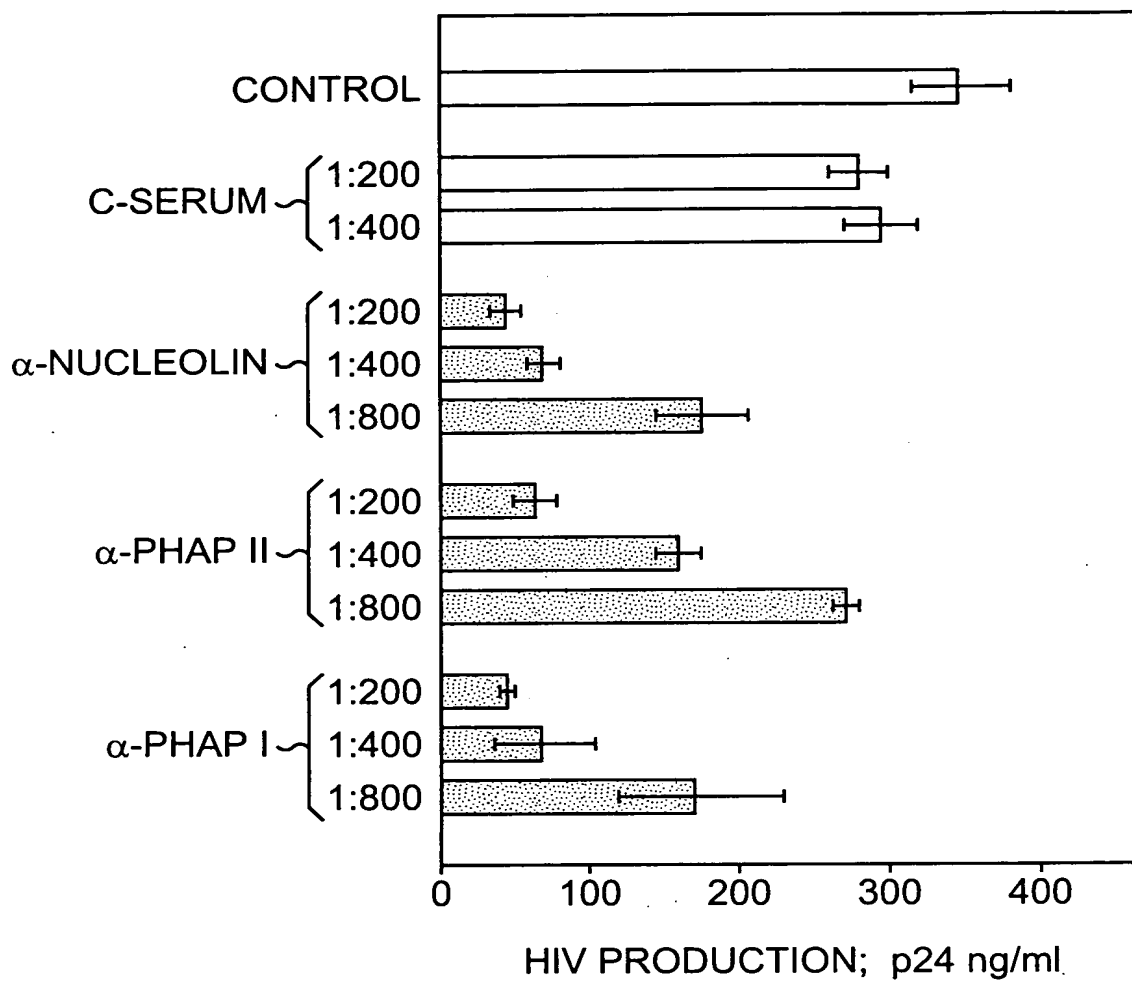


FIG. 15



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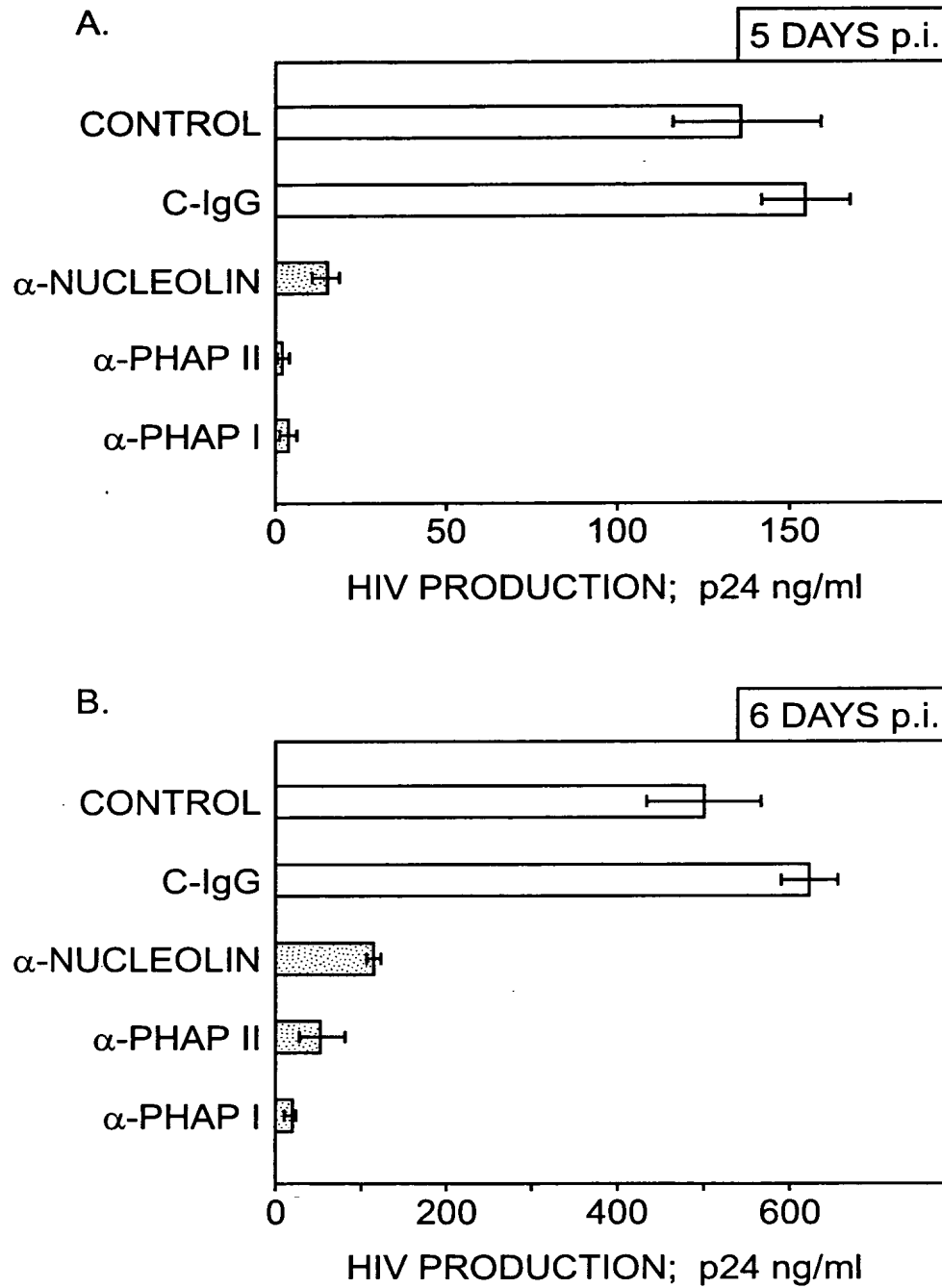


FIG. 16



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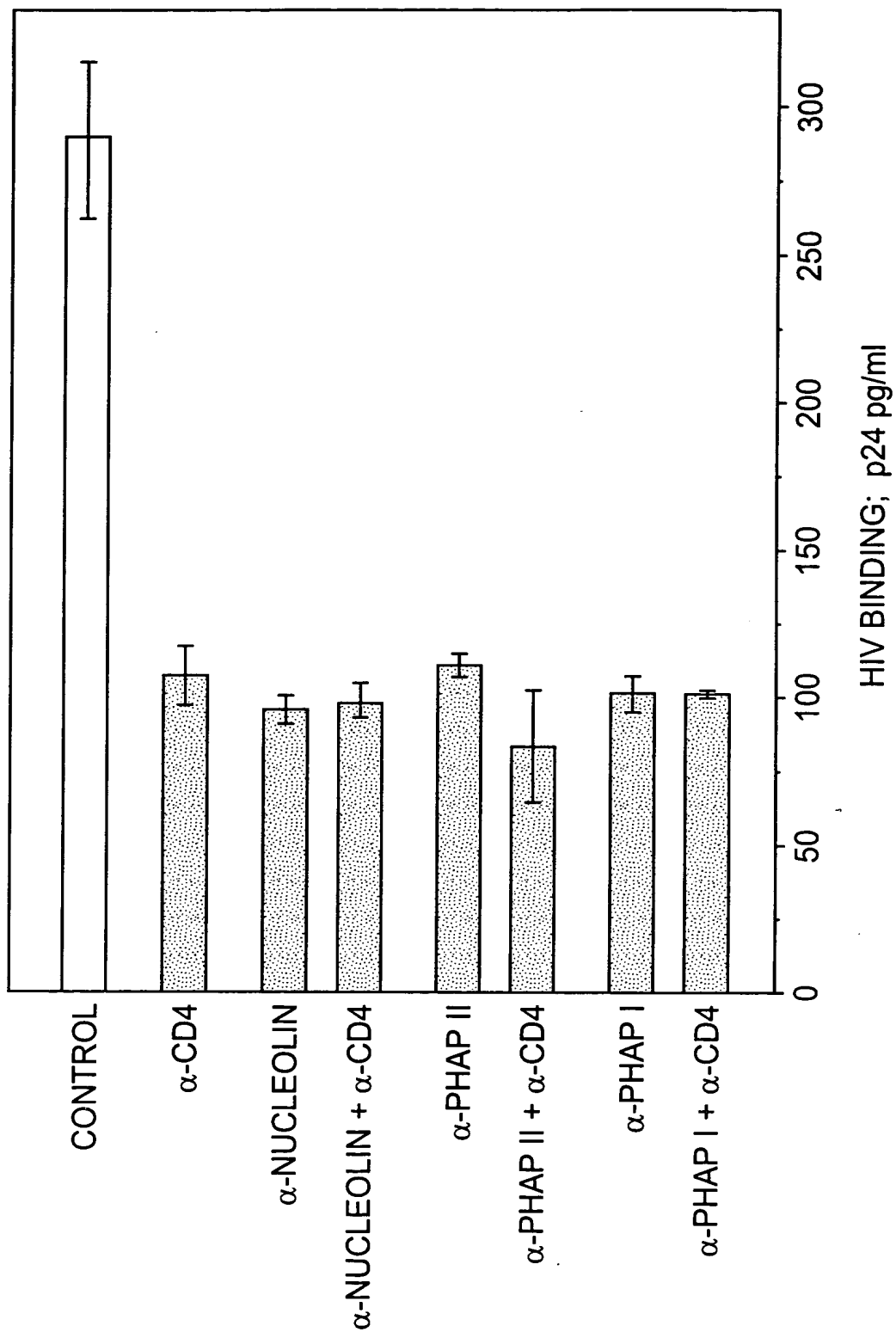


FIG. 17



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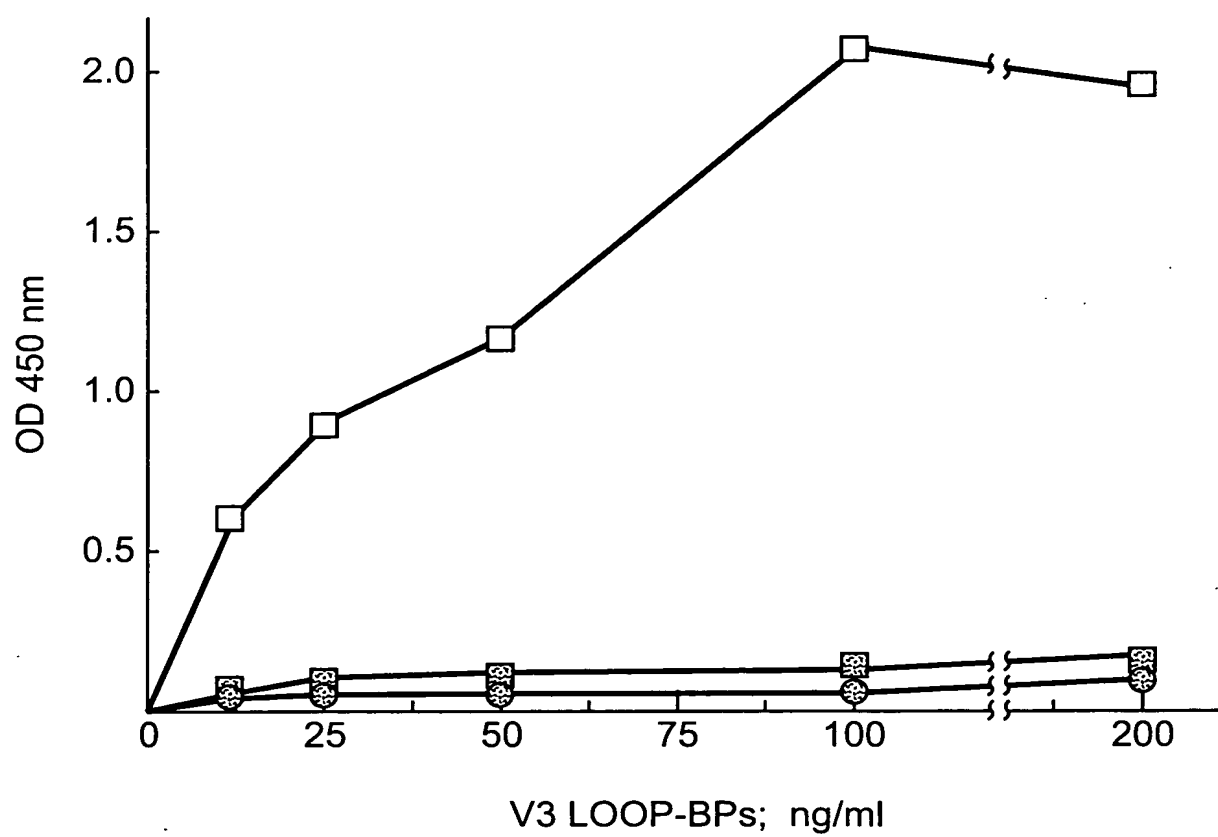
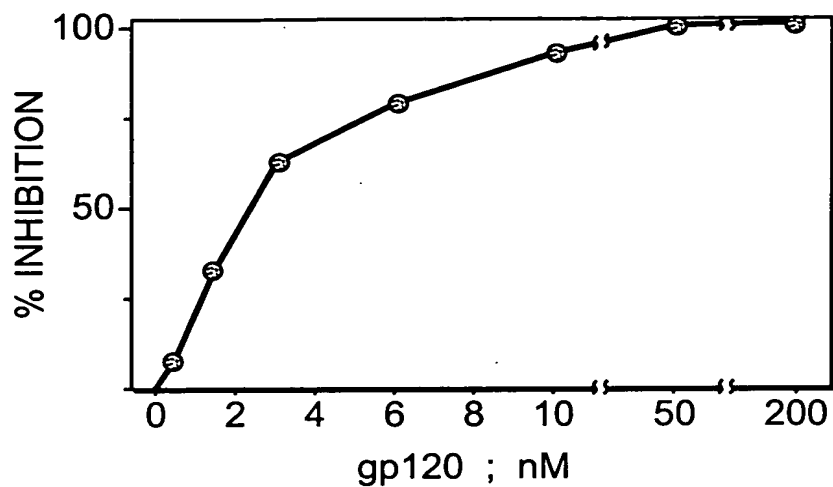


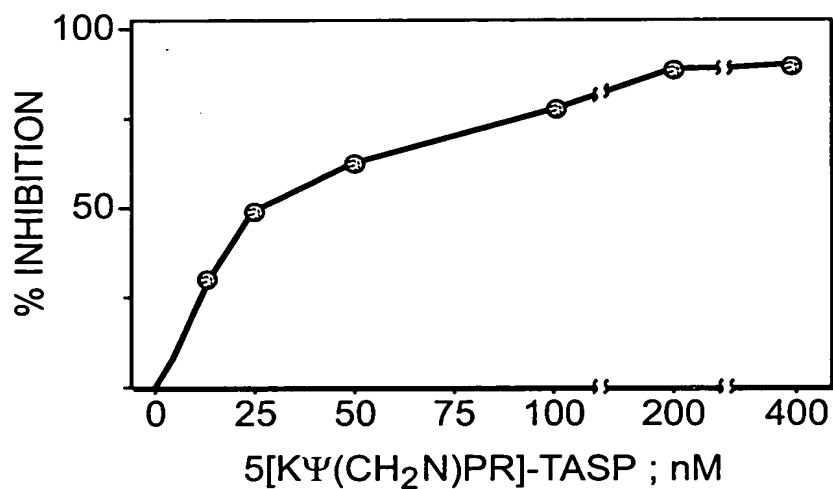
FIG. 18

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A. 5[KΨ(CH₂N)PR] -TASP BINDING TO THE V3 LOOP-BPs



B. gp120 BINDING TO THE V3 LOOP-BPs



C. gp120 BINDING TO THE V3 LOOP-BPs

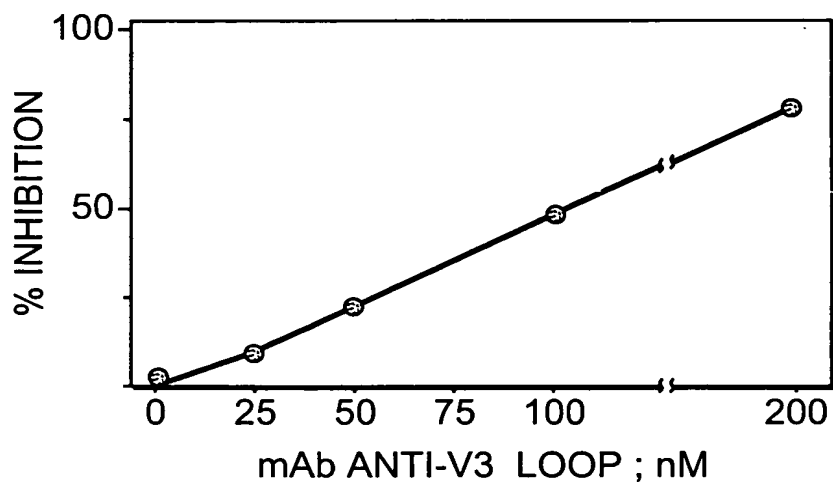
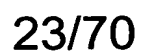


FIG. 19



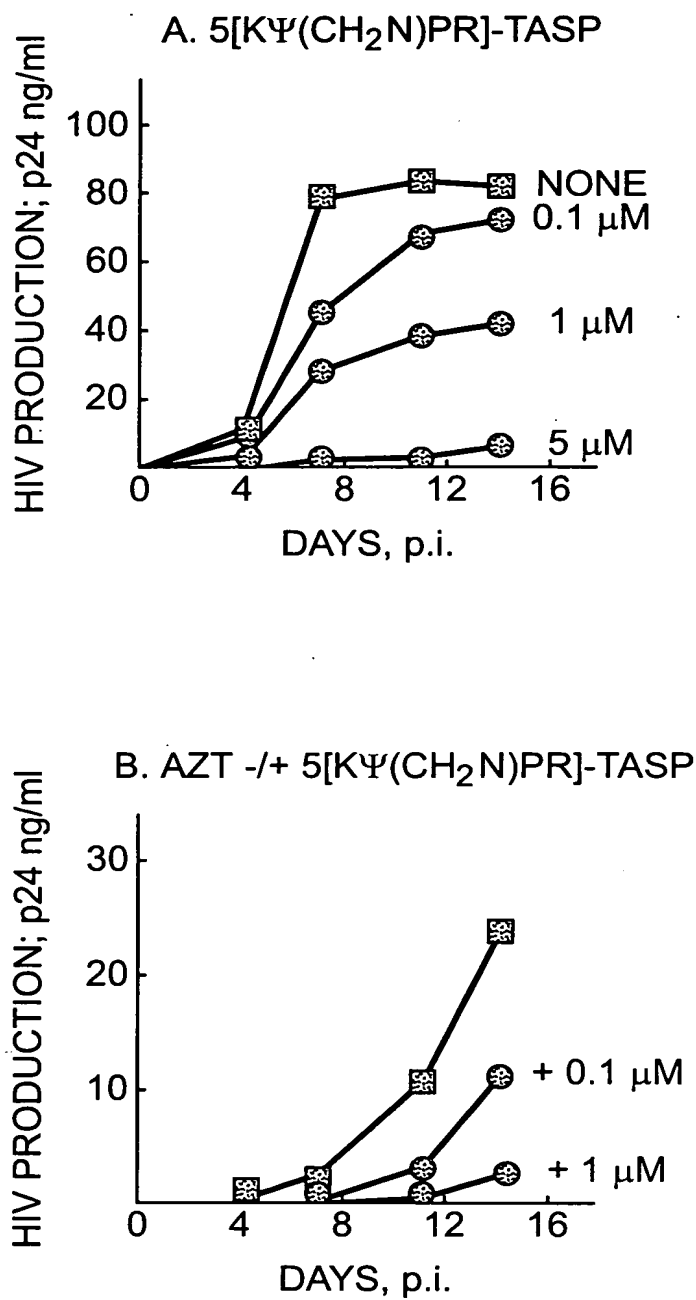


FIG. 21

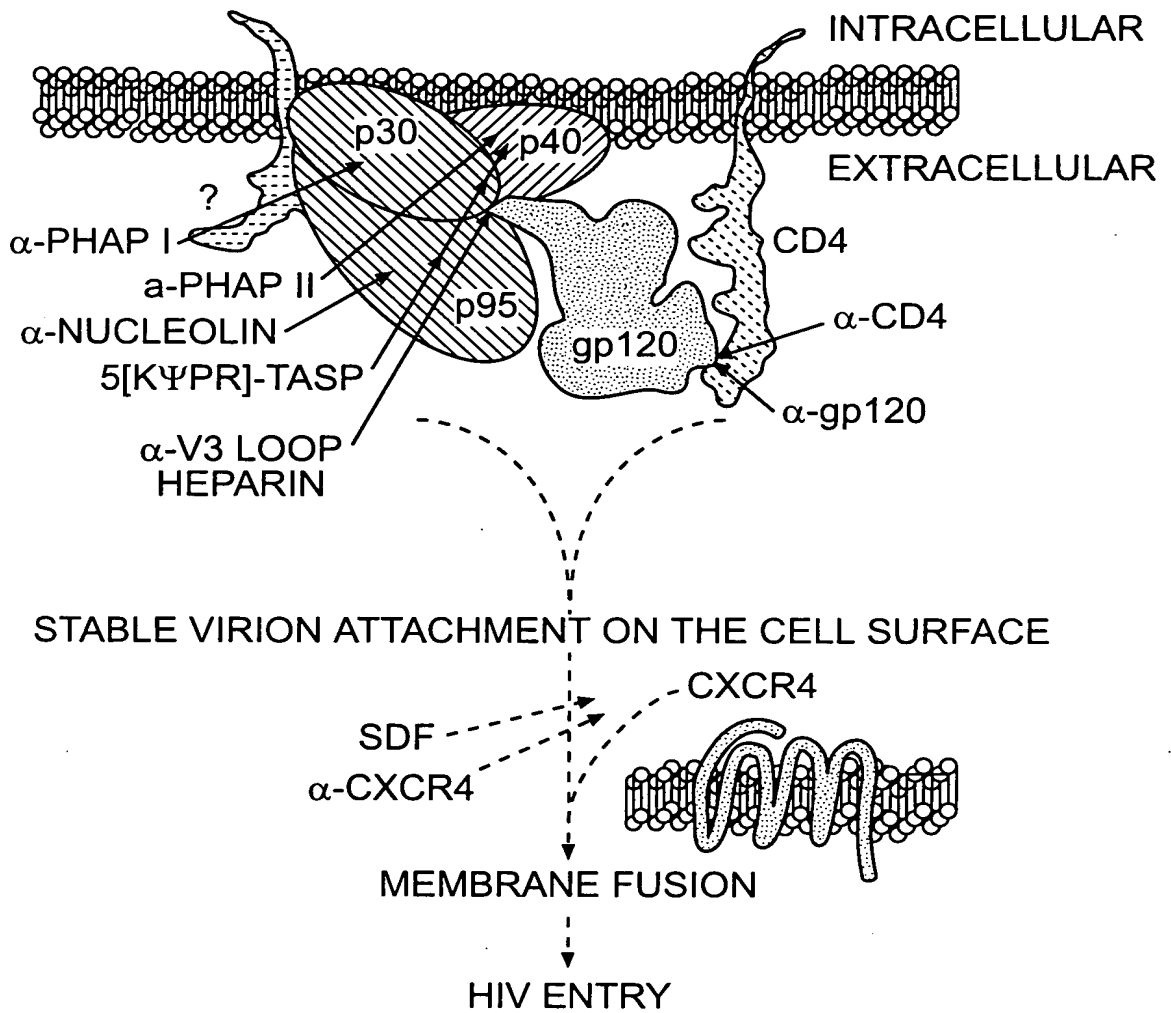


FIG. 22



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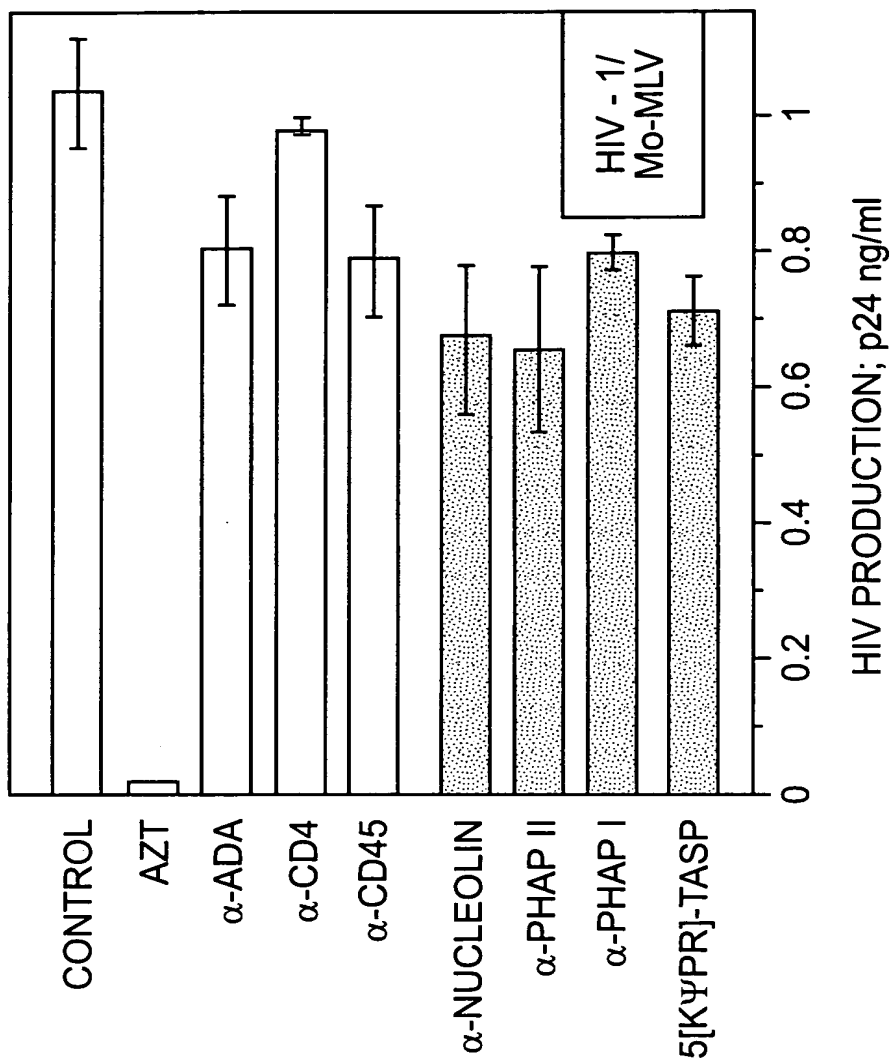


FIG. 23

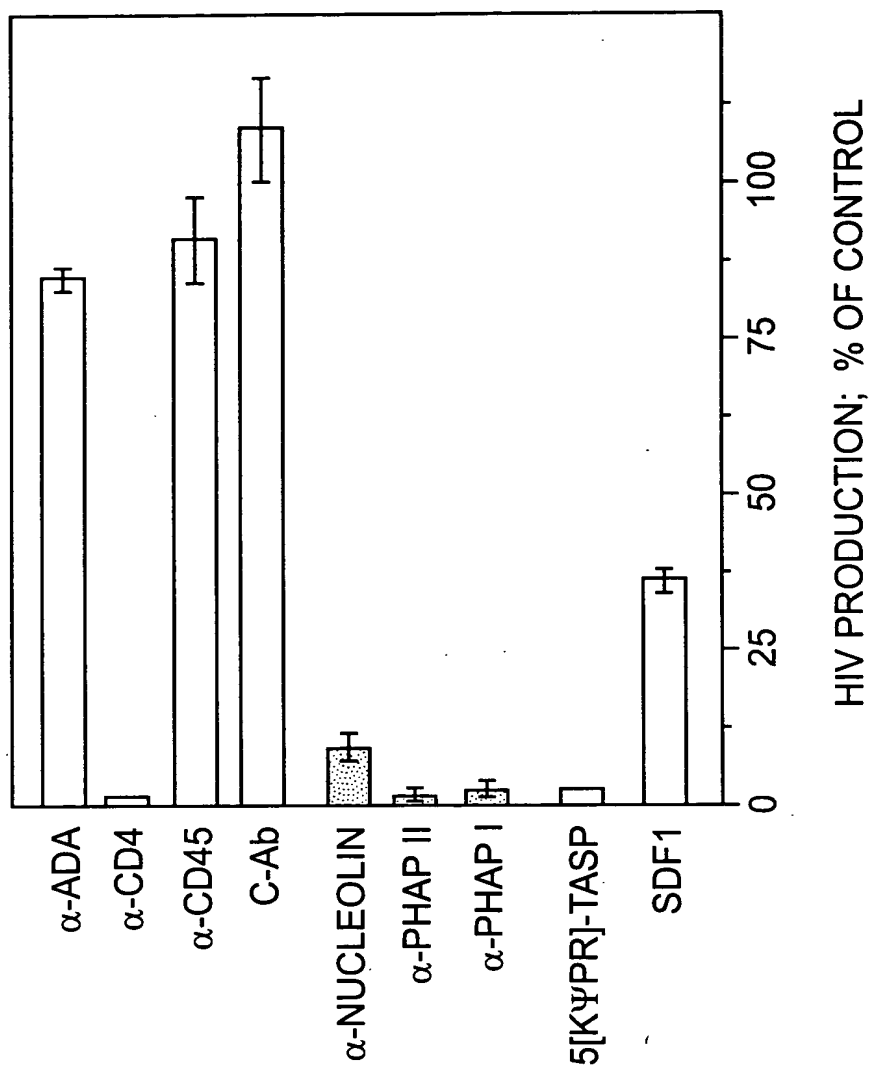


FIG. 24

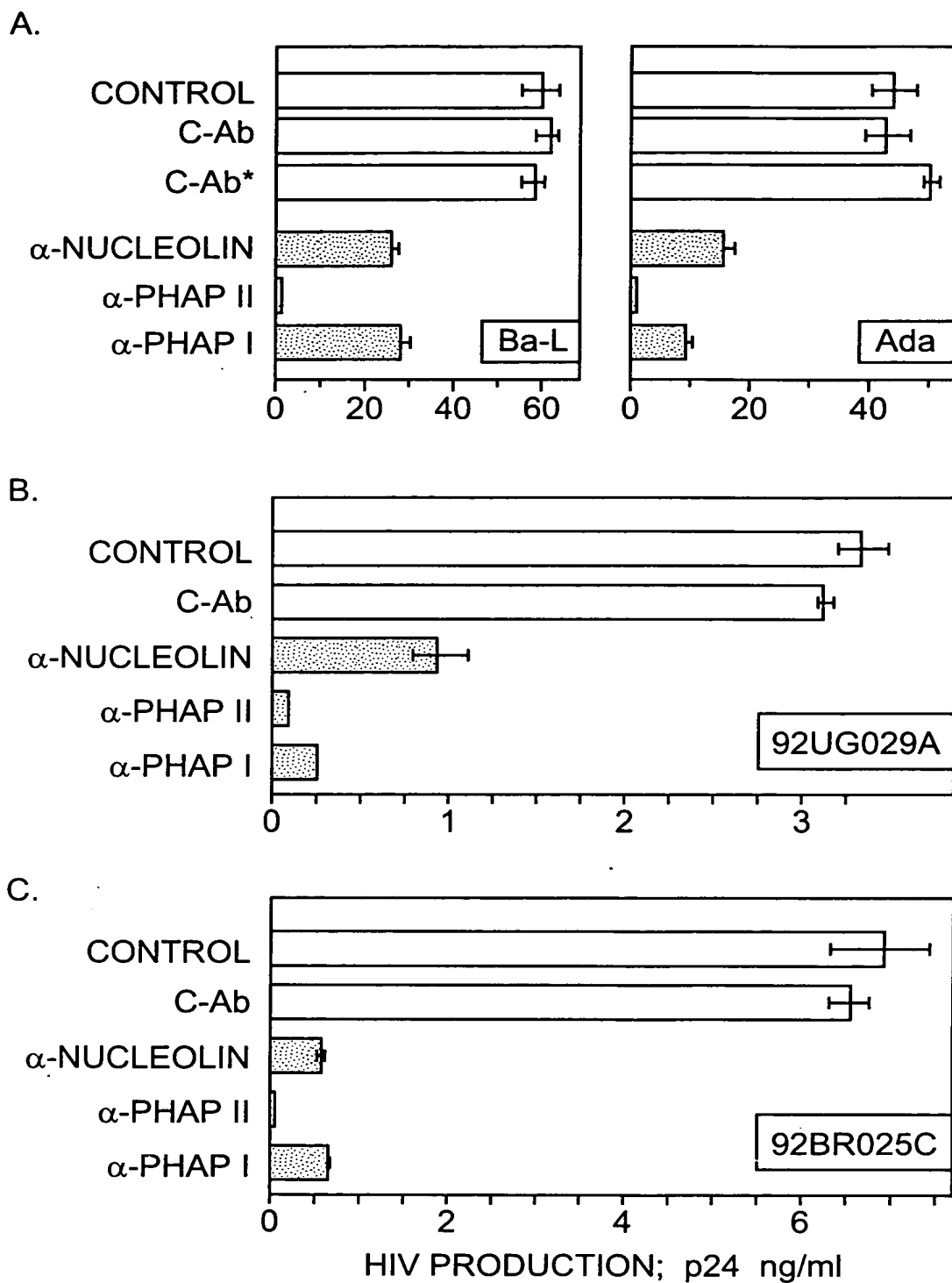


FIG. 25

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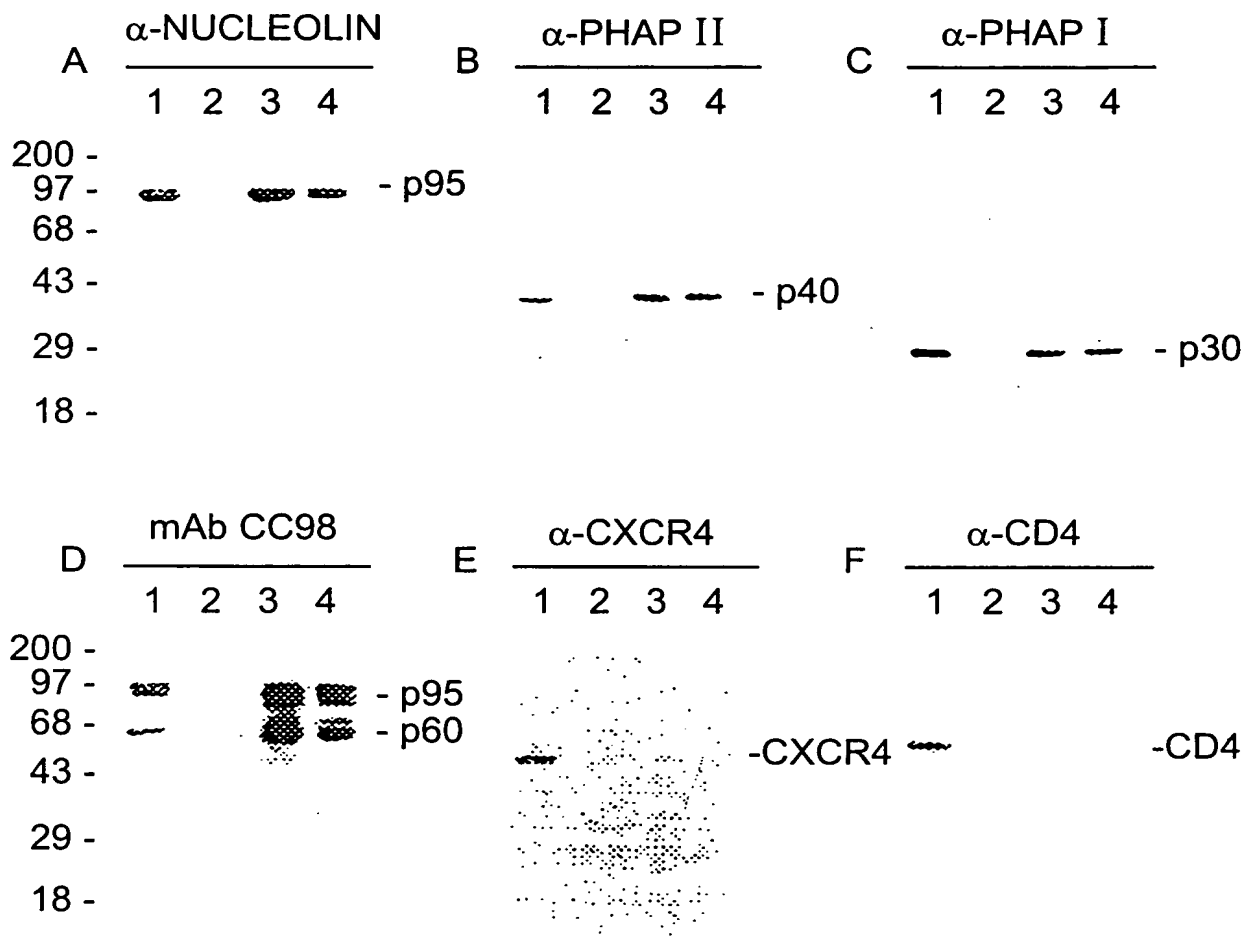


FIG. 26



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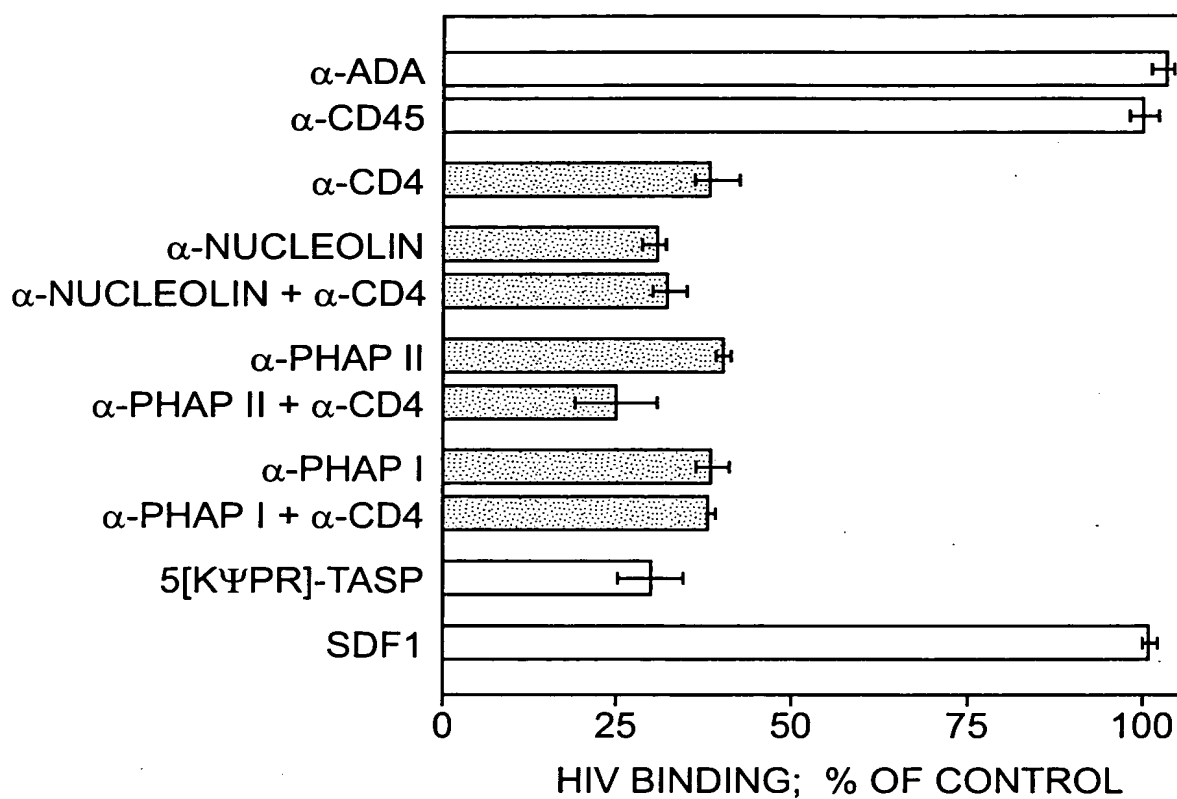


FIG. 27

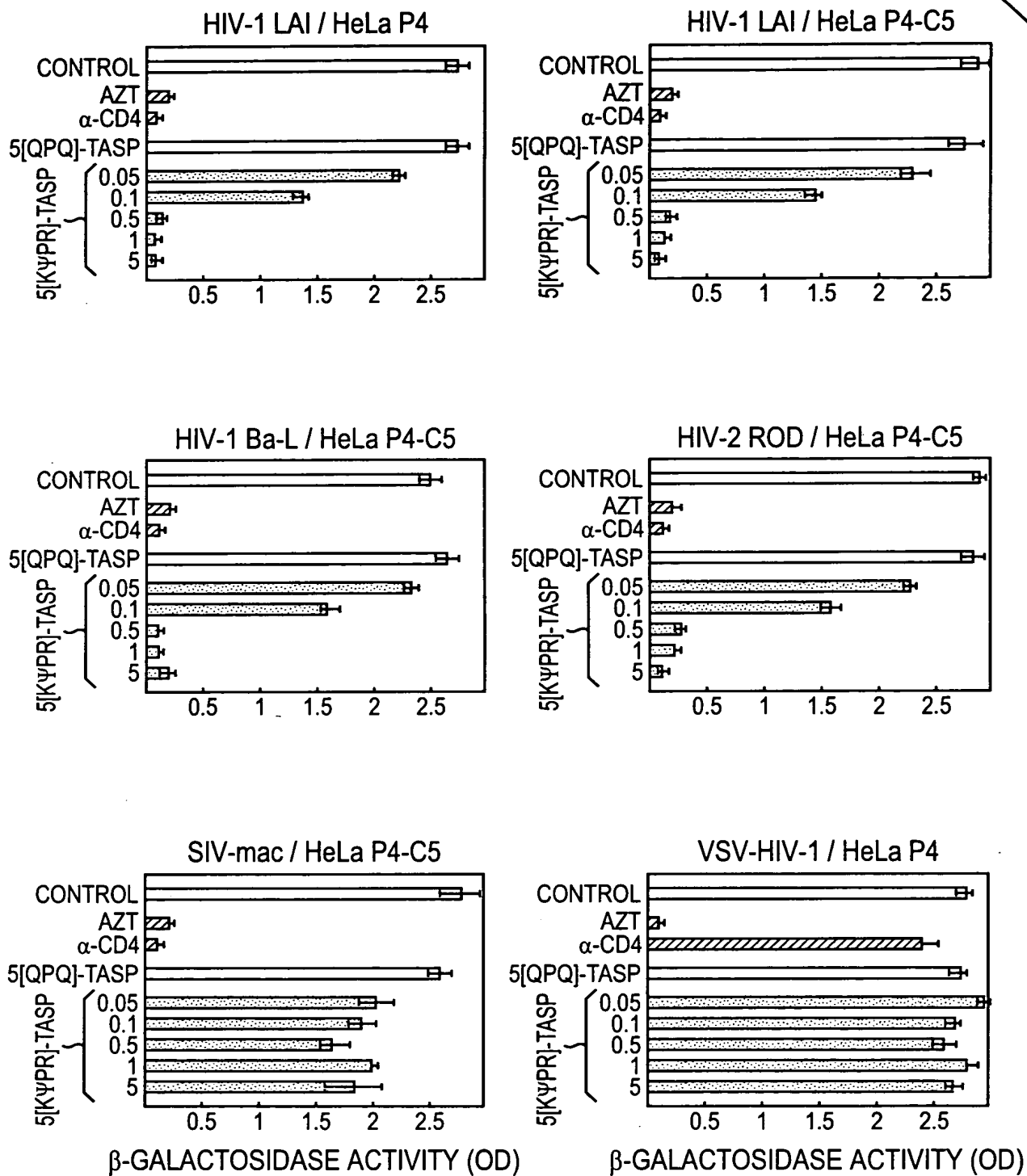


FIG. 28

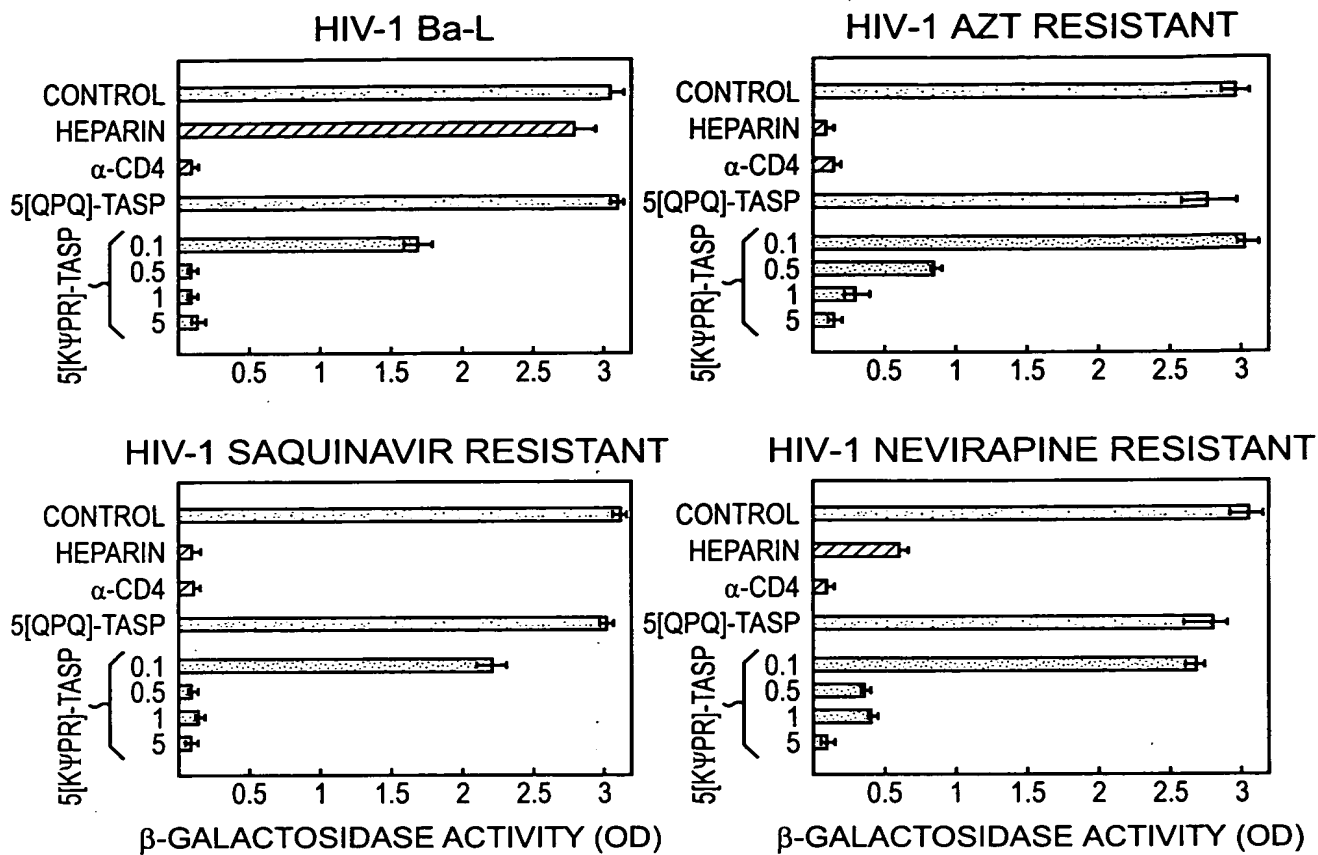


FIG. 29

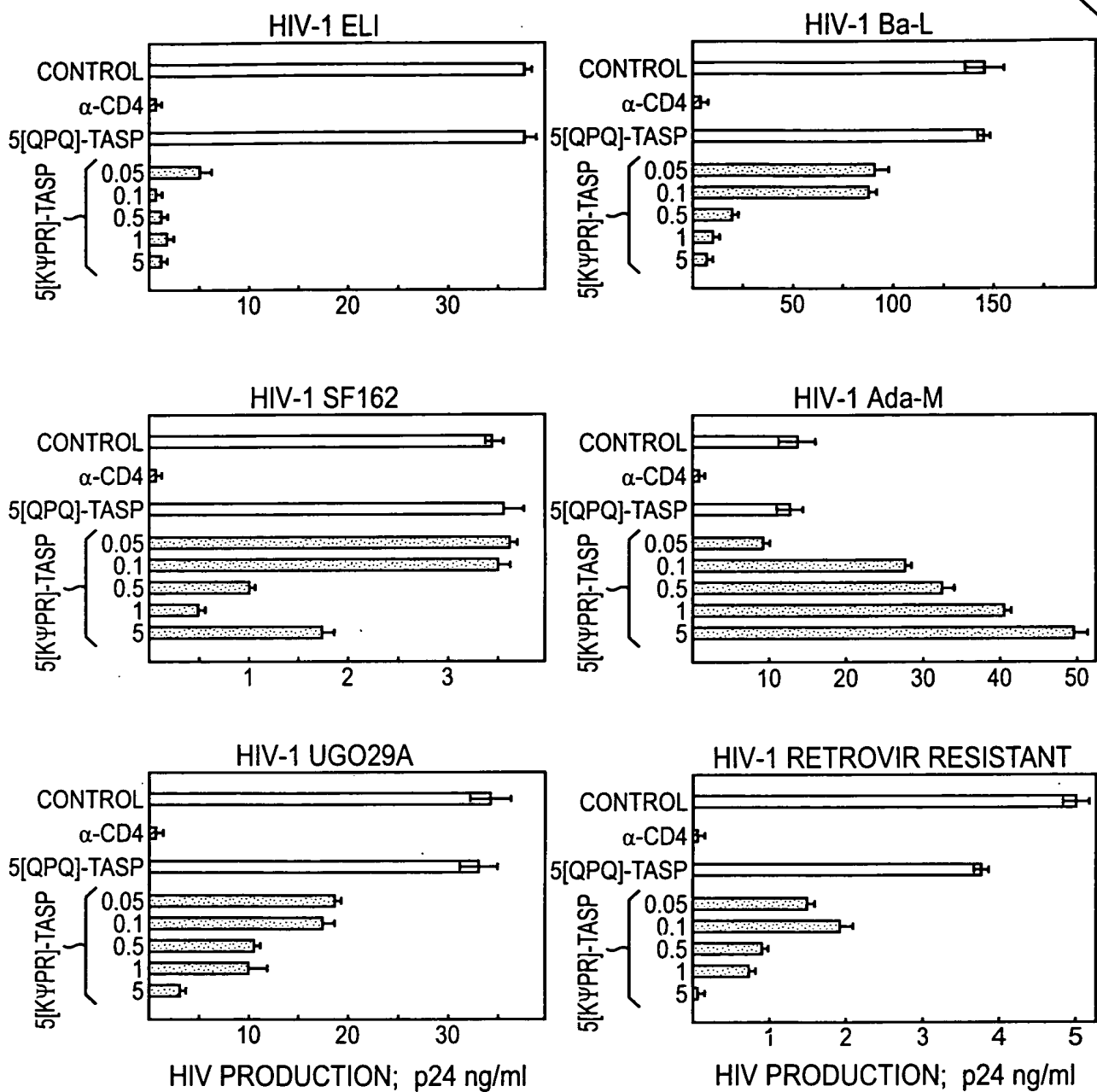


FIG. 30

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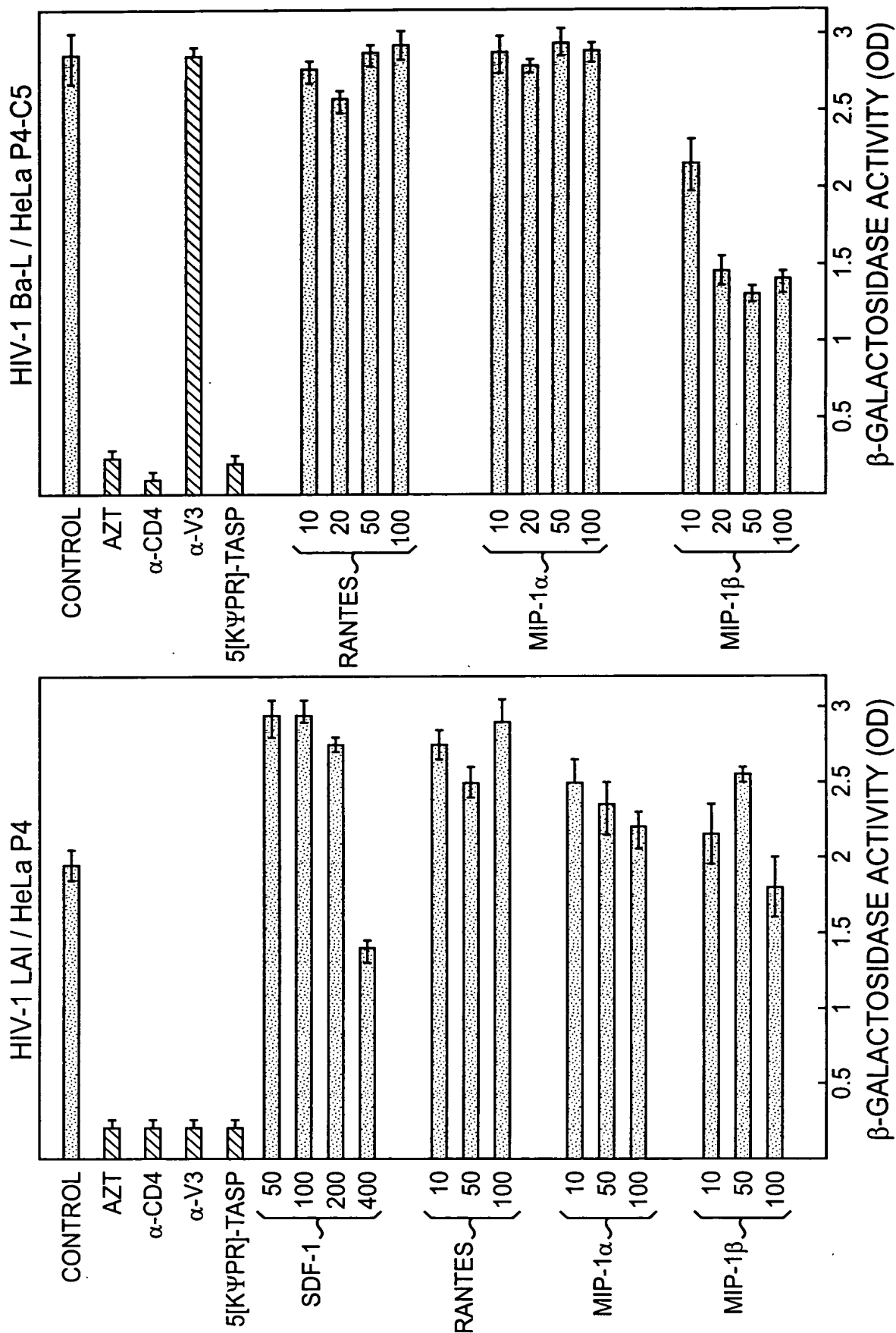


FIG. 31

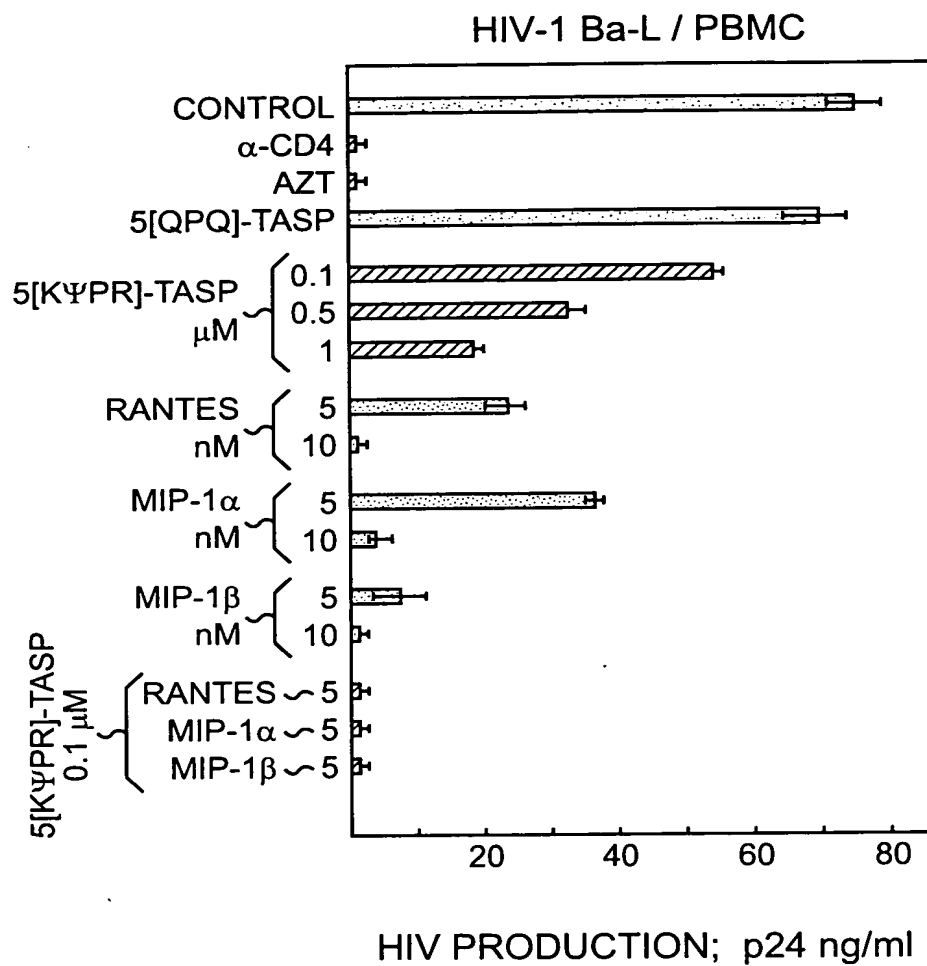


FIG. 32

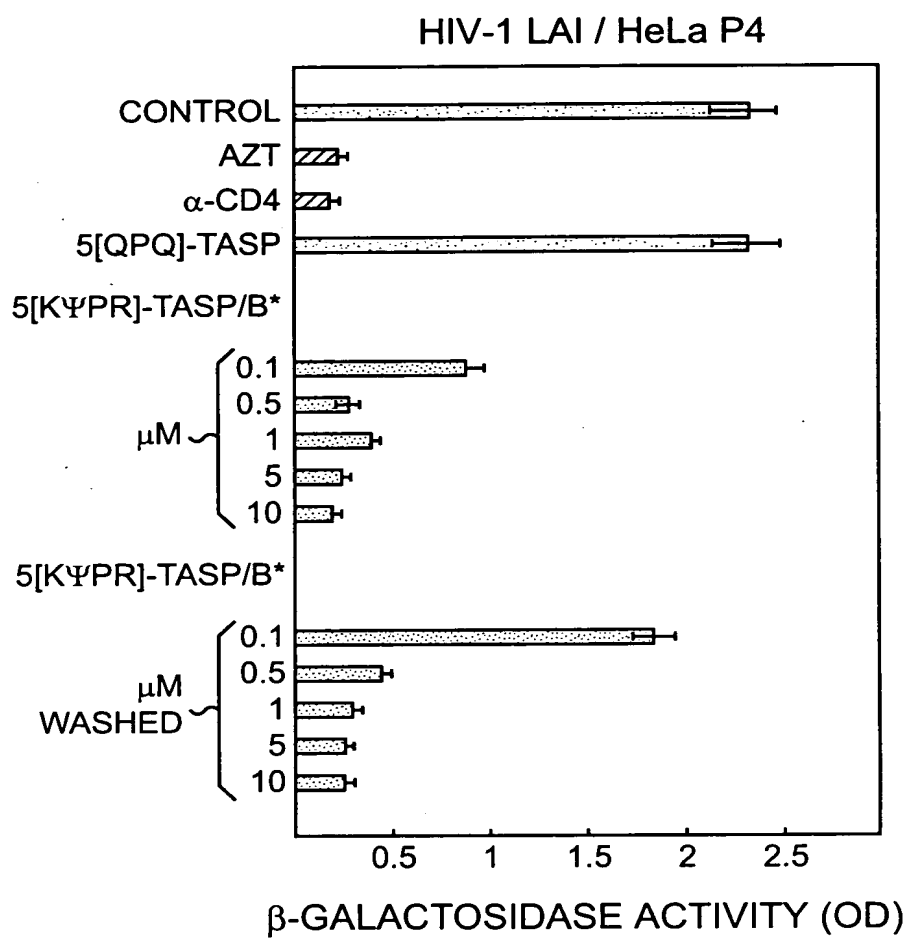


FIG. 33

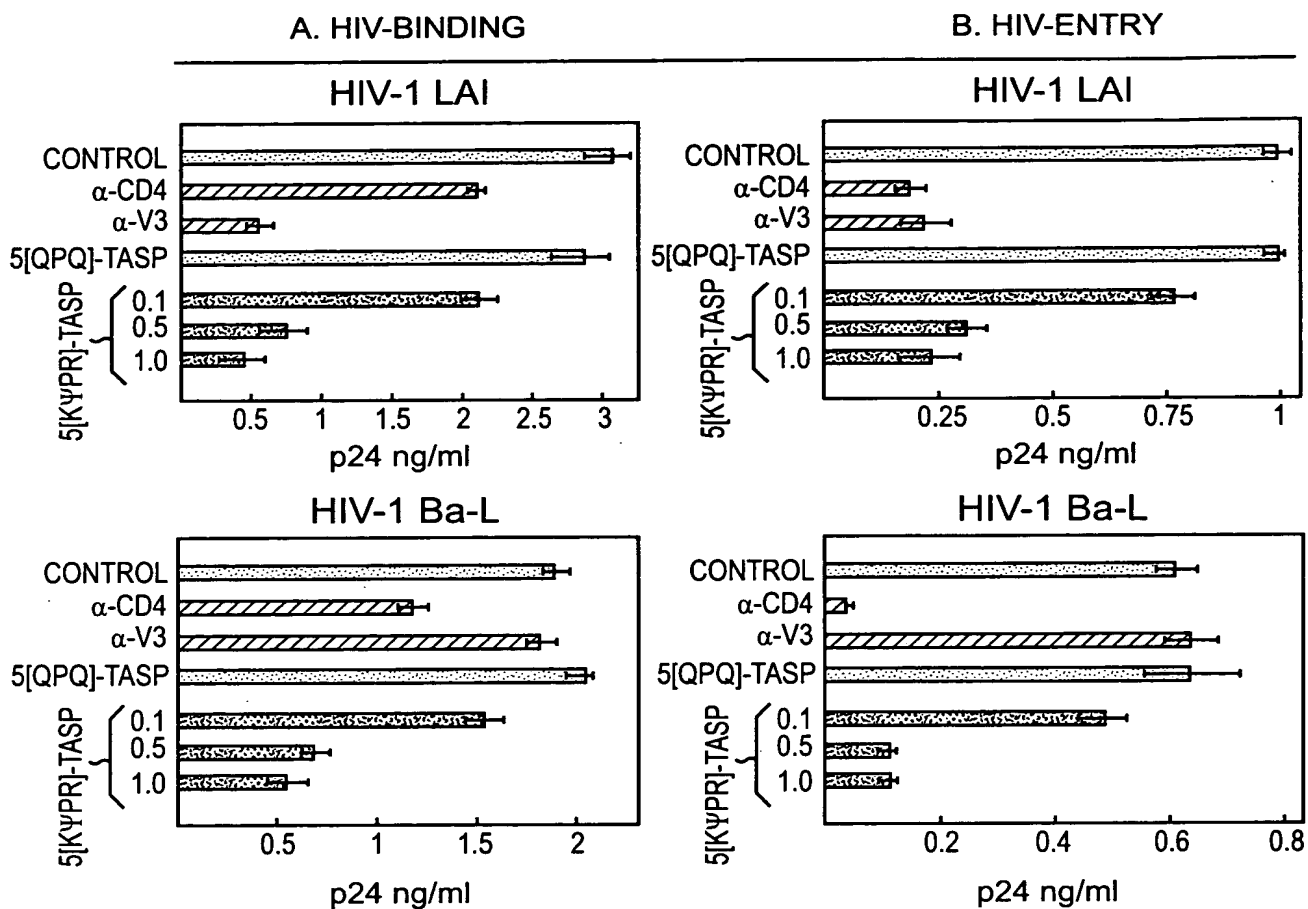


FIG. 34



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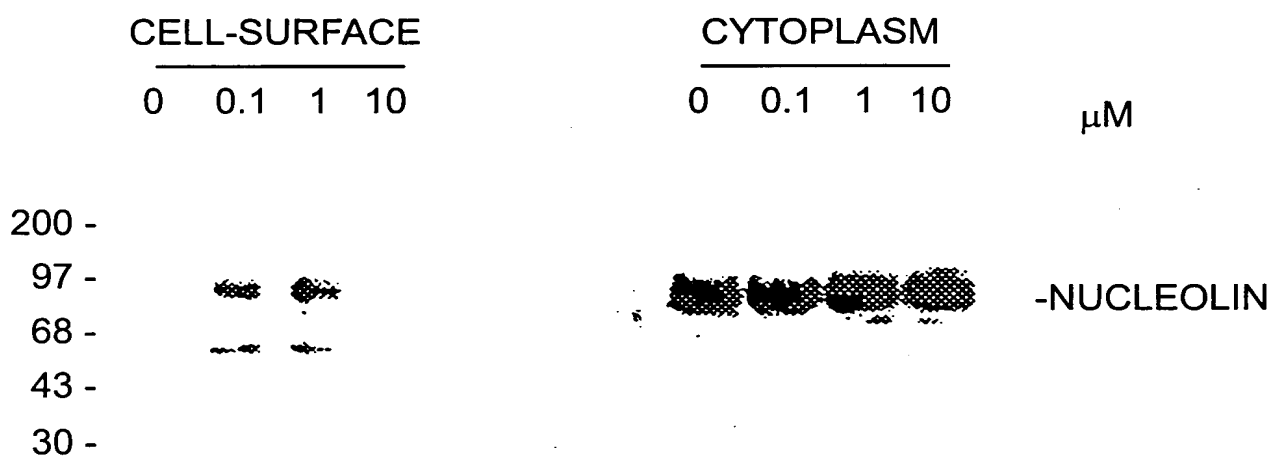


FIG. 35



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CELL-SURFACE

1 2 3 4



-NUCLEOLIN (p95)

1: 1hr; 2: 1hr; 3: 6hr; 4: 24hr;
2, 3, 4: 5 μ M

FIG. 36

THE EFFECT OF HEPARIN AT $\mu\text{g/ml}$ ON HIV INFECTION IN HeLa P4-C5 CELLS.

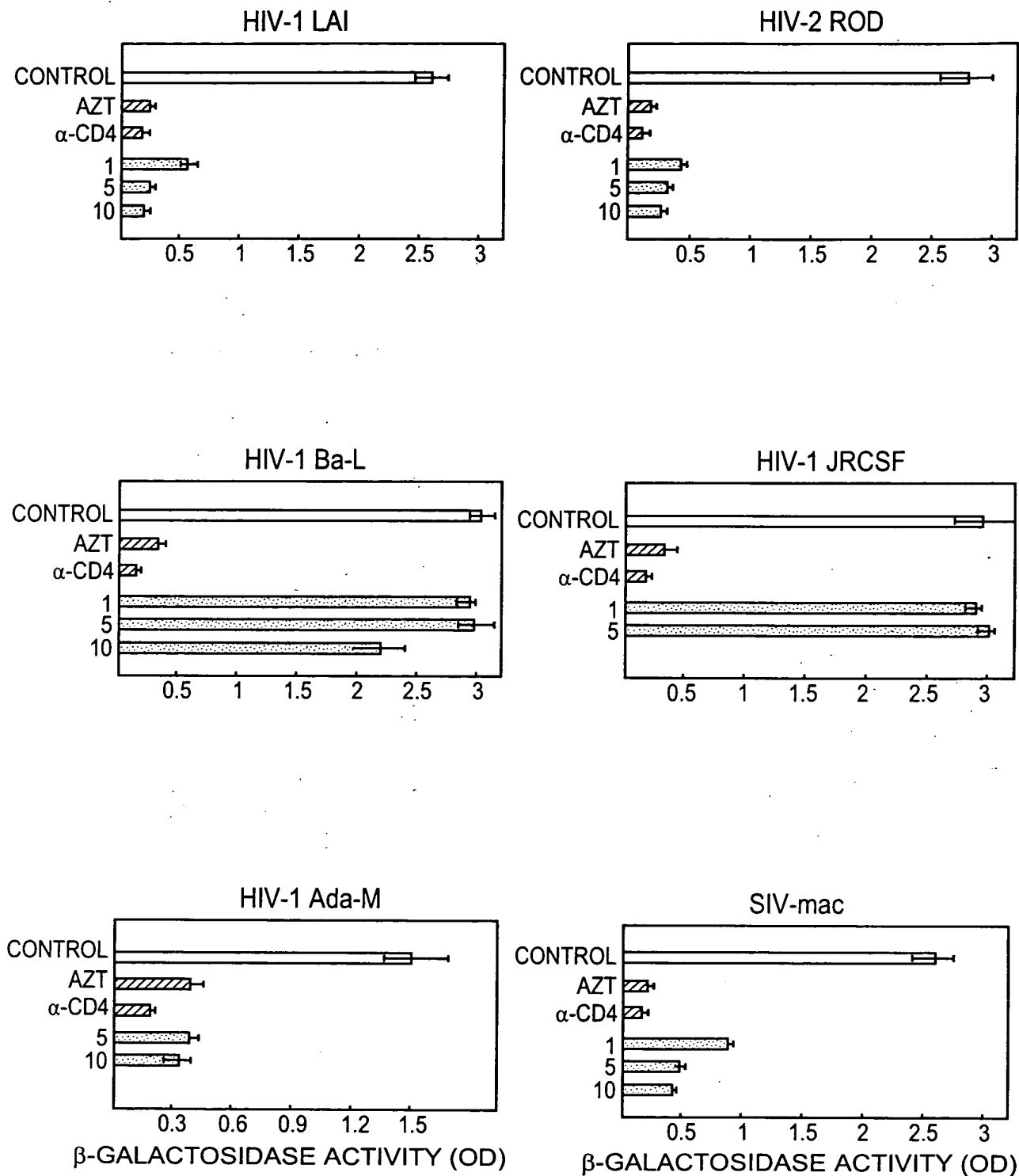


FIG. 37



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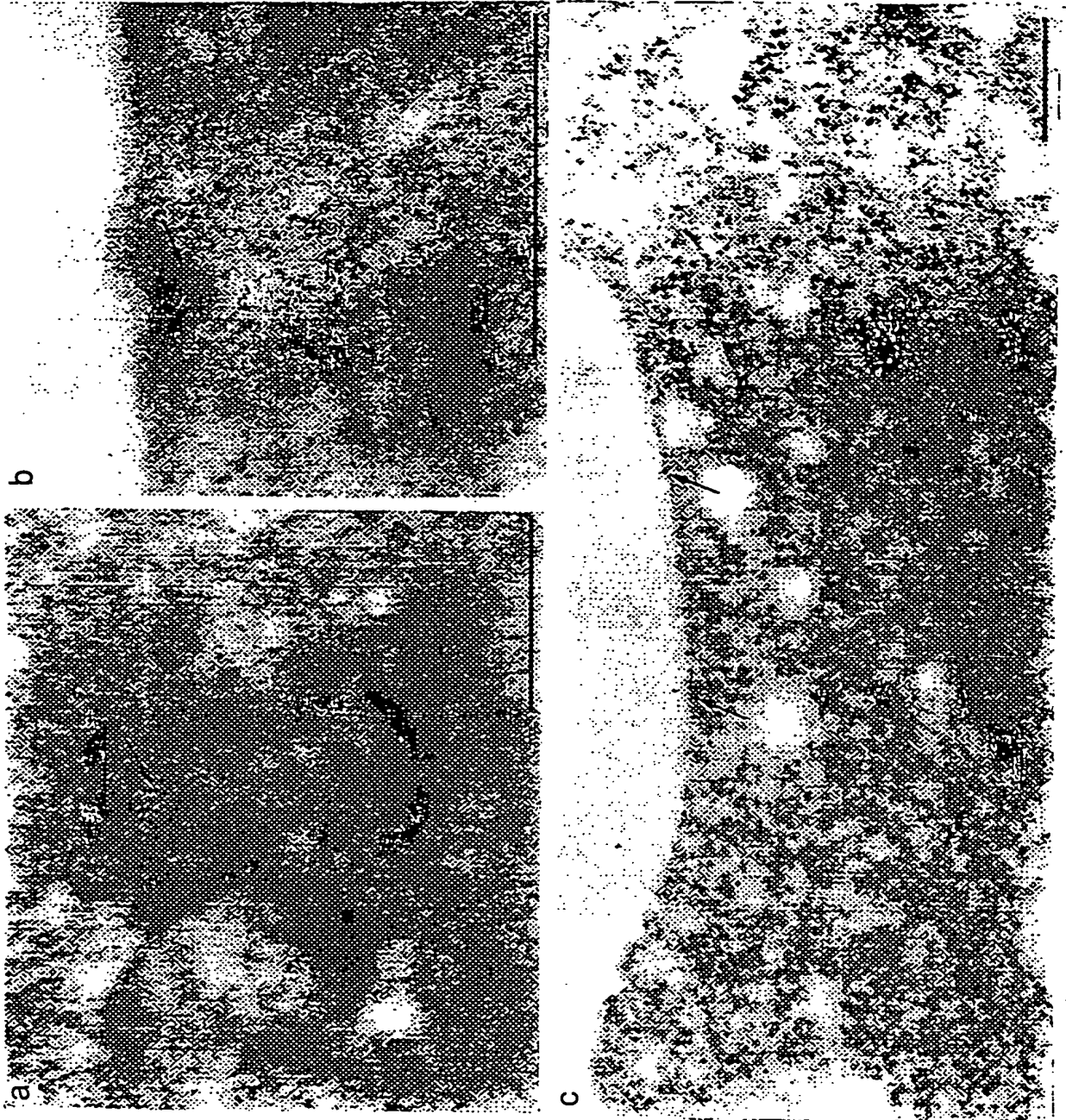


FIG. 38



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FIG. 39



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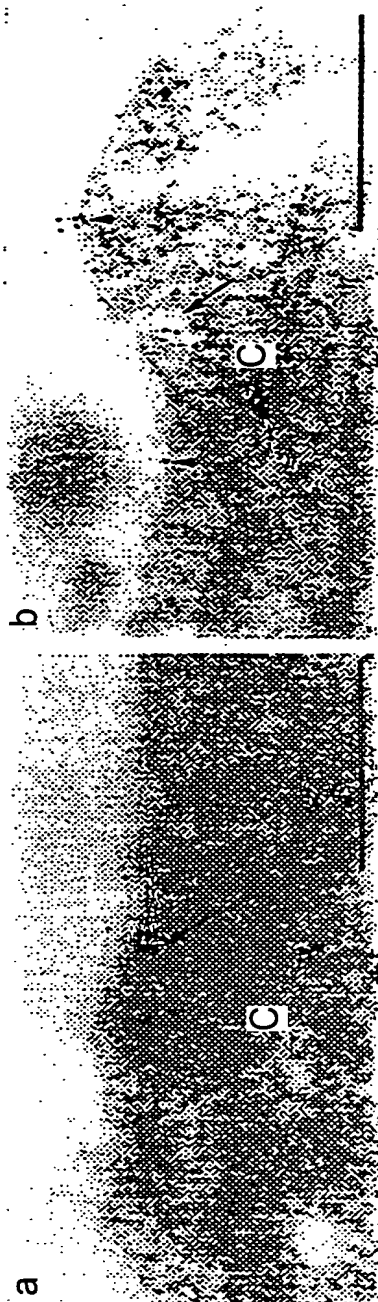


FIG. 40A



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FIG. 40B

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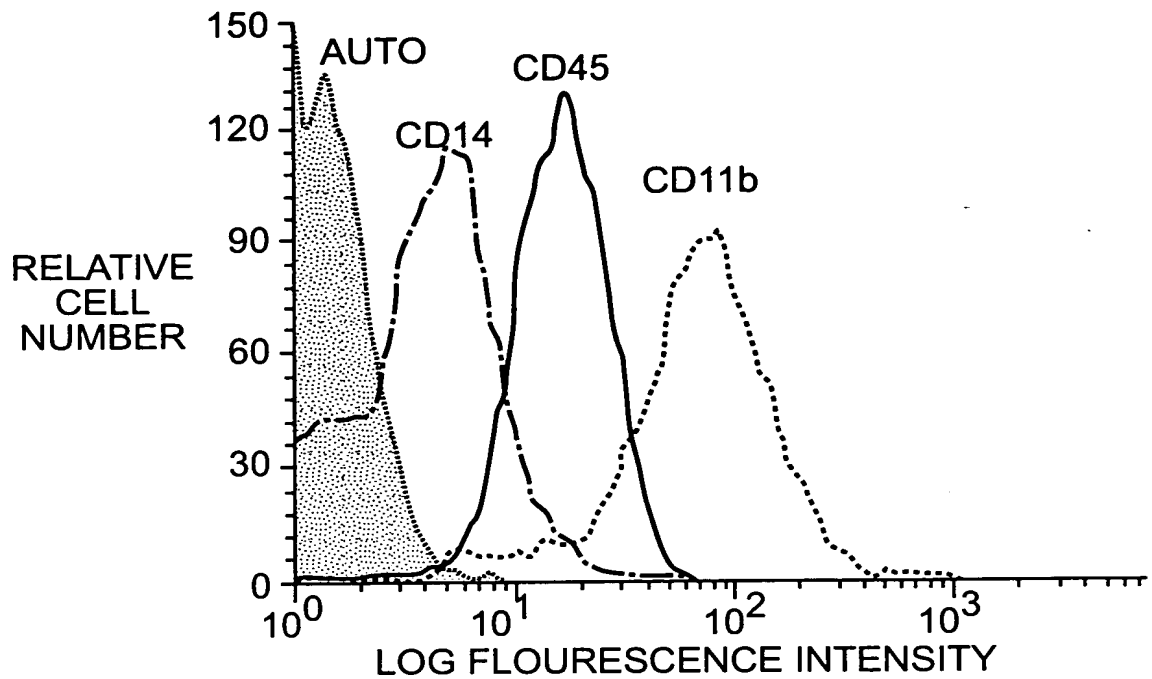


FIG. 41A

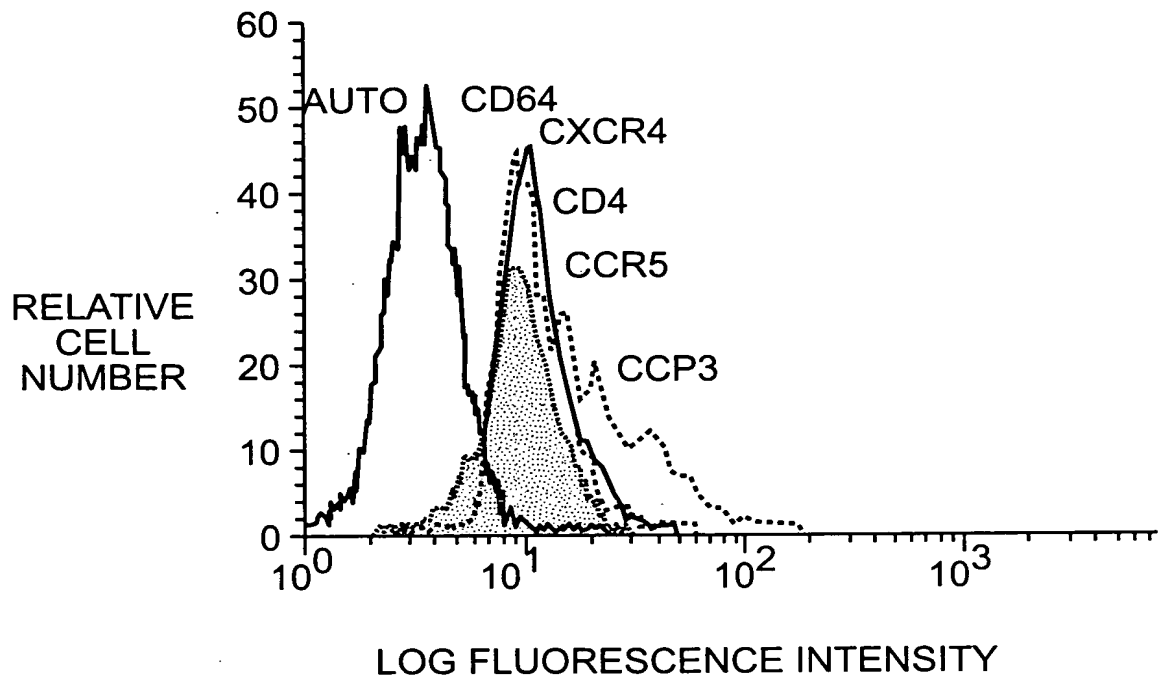


FIG. 41B

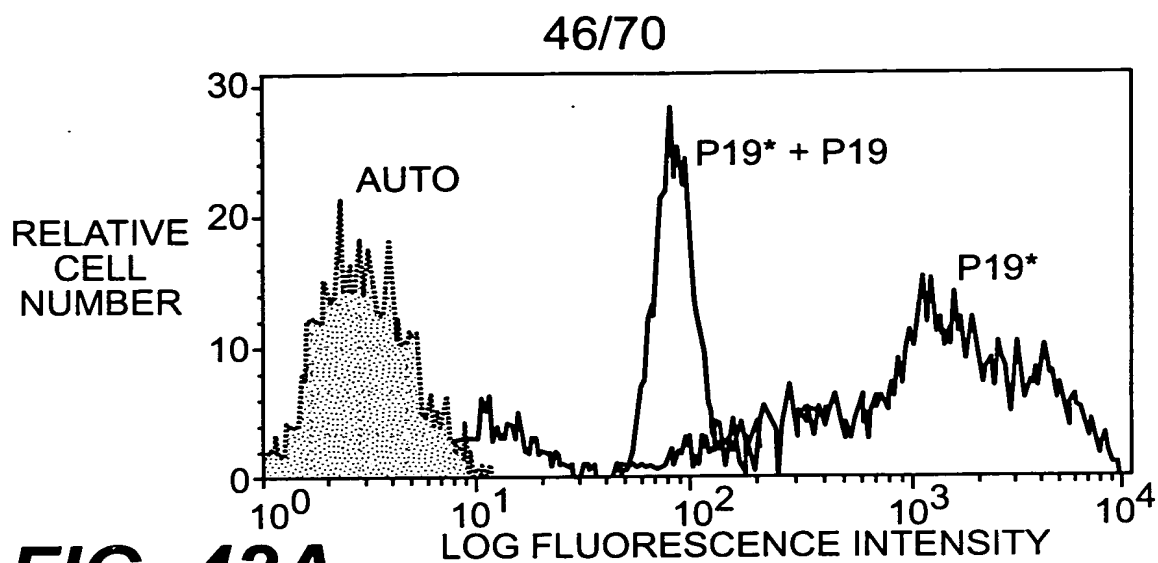


FIG. 42A

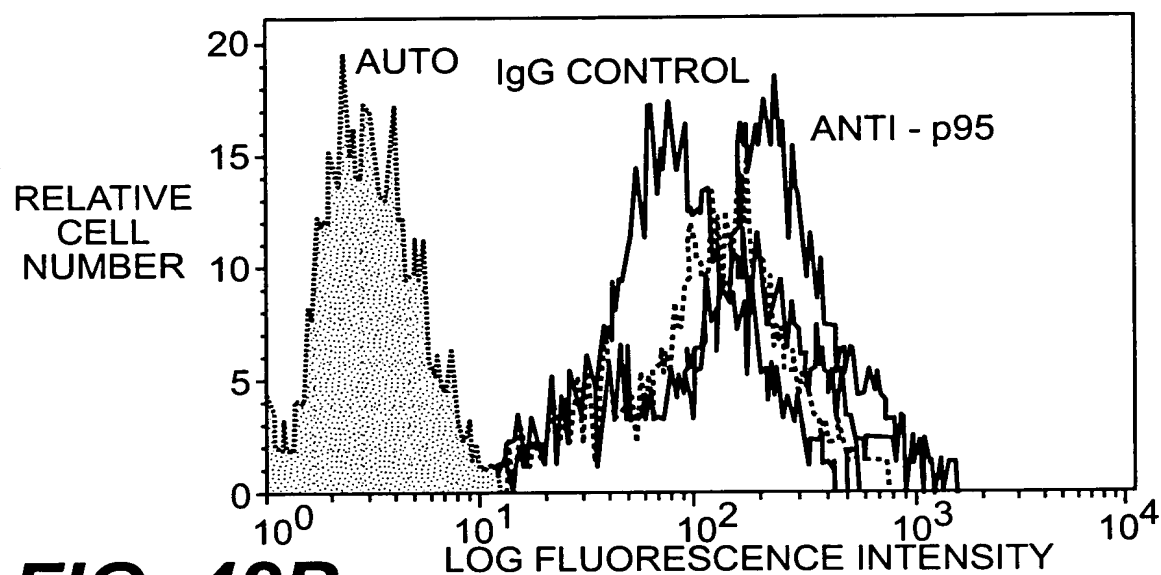


FIG. 42B

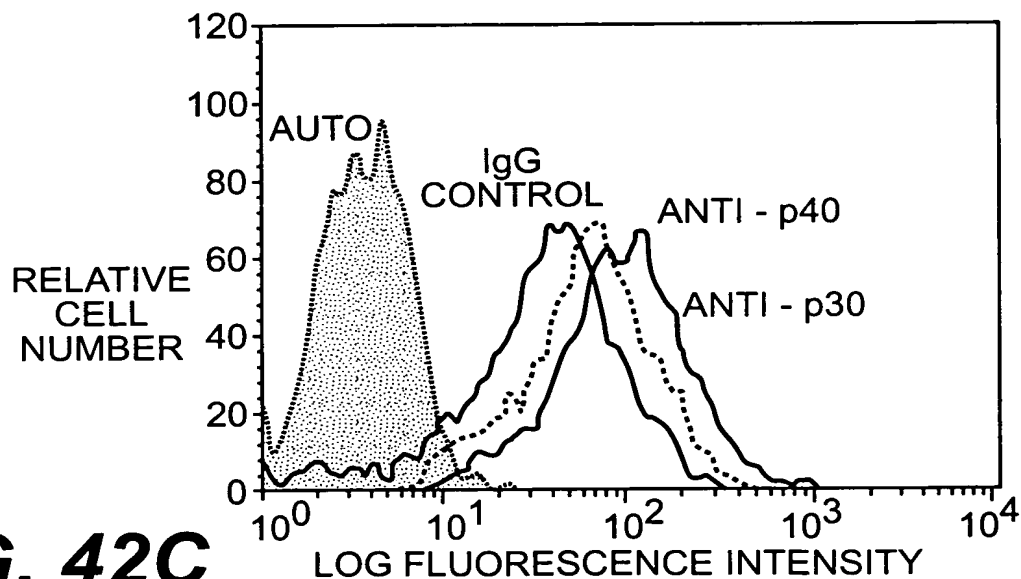


FIG. 42C



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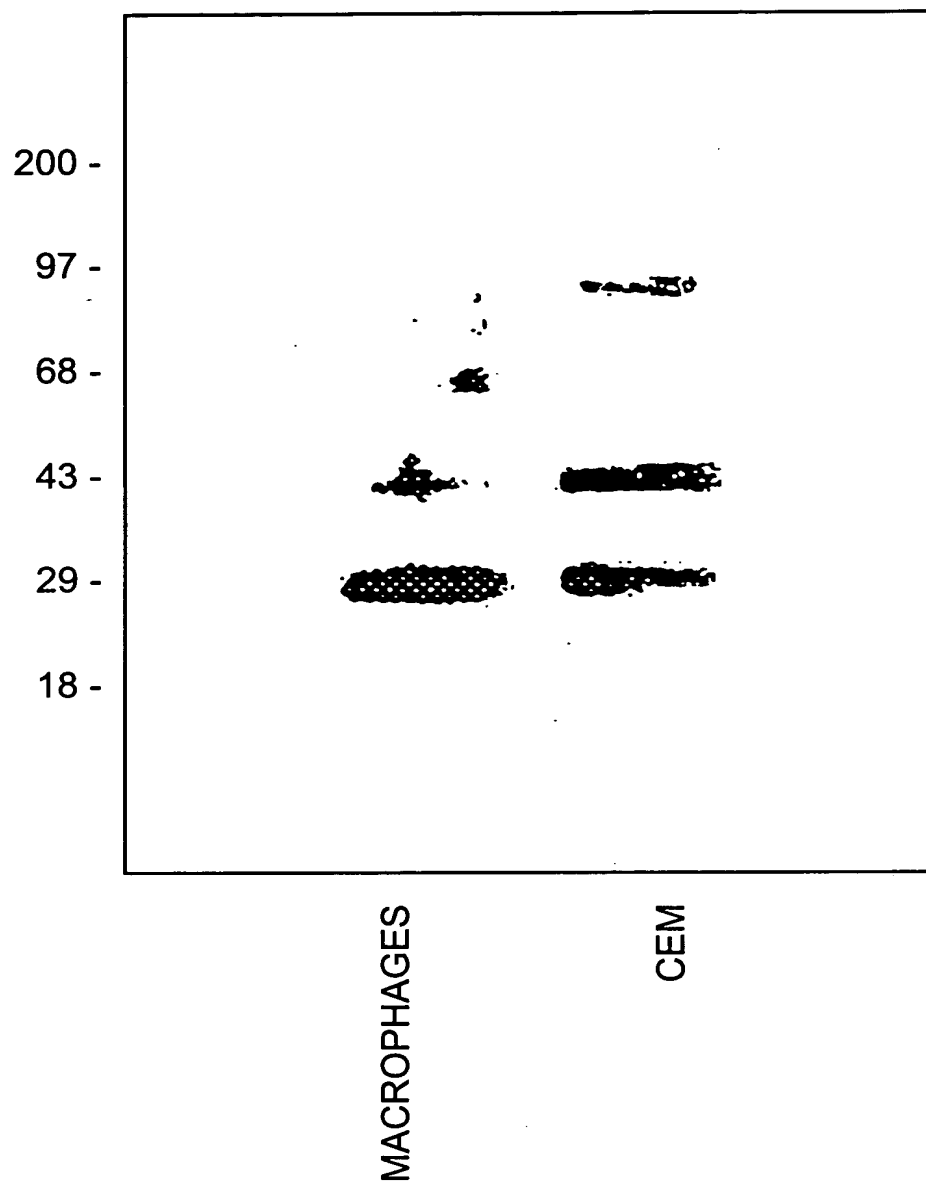


FIG. 43

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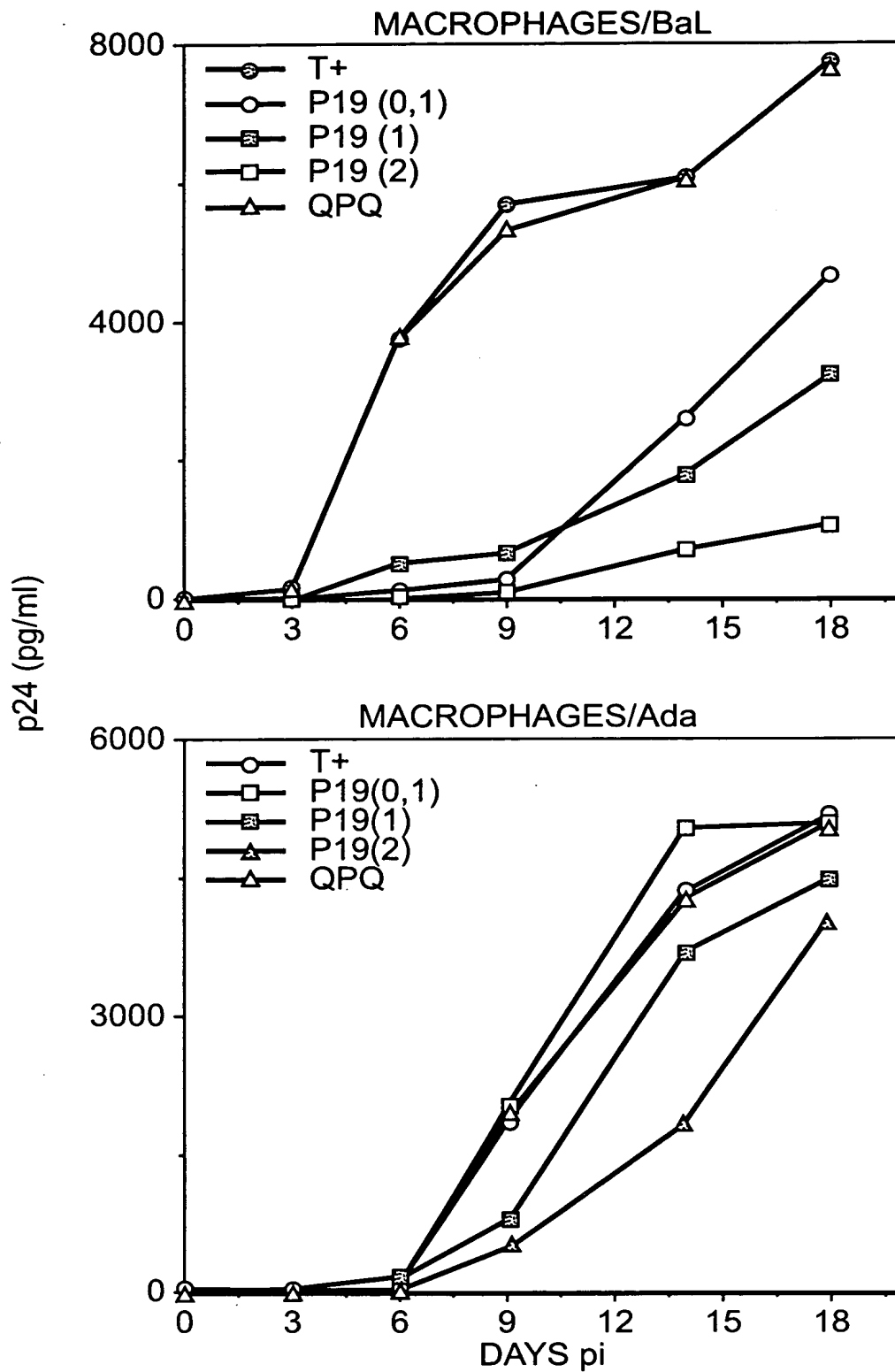


FIG. 44



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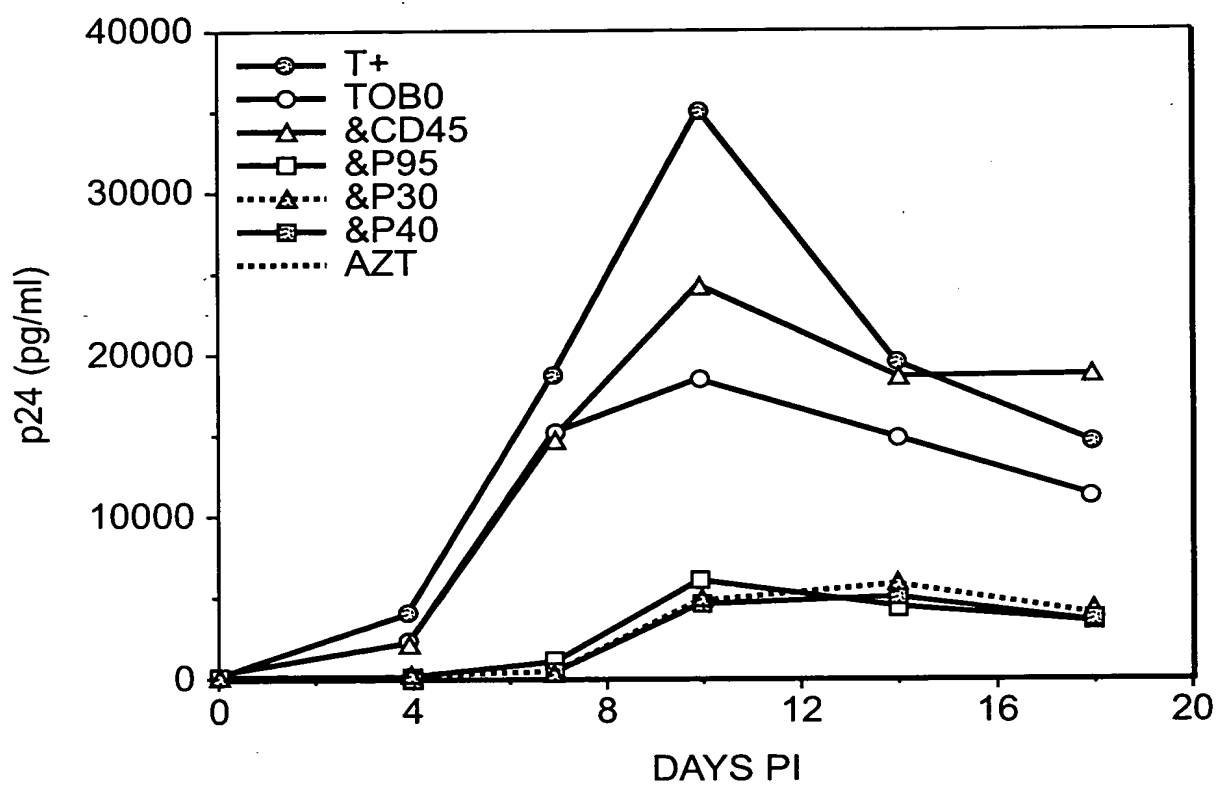
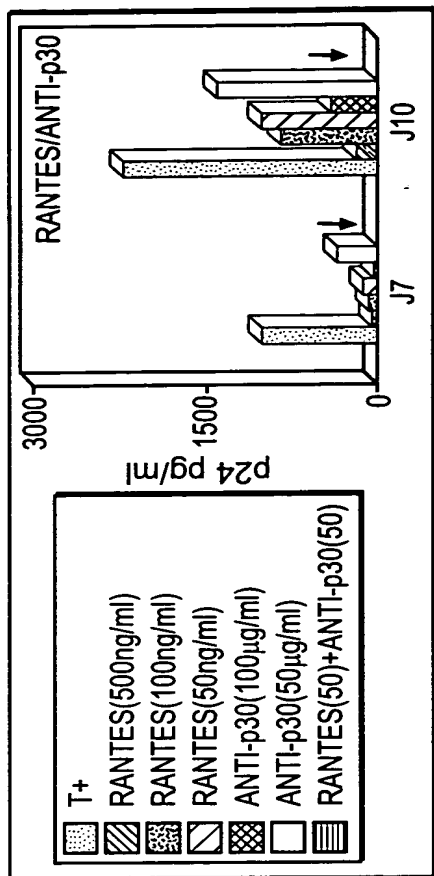
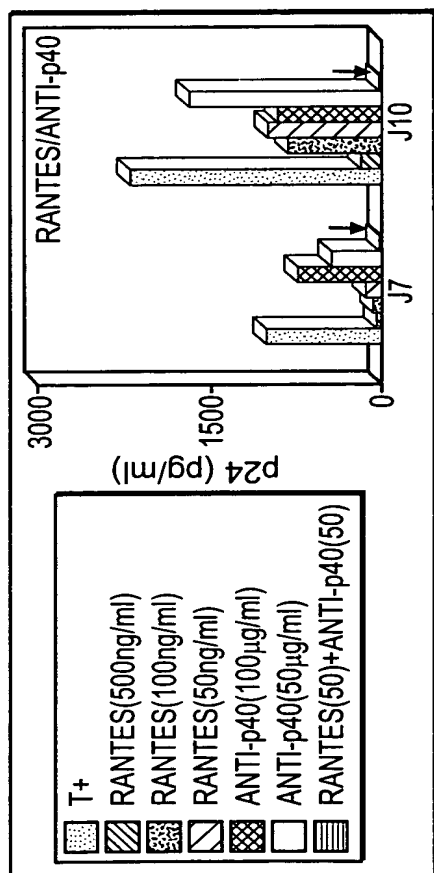


FIG. 45



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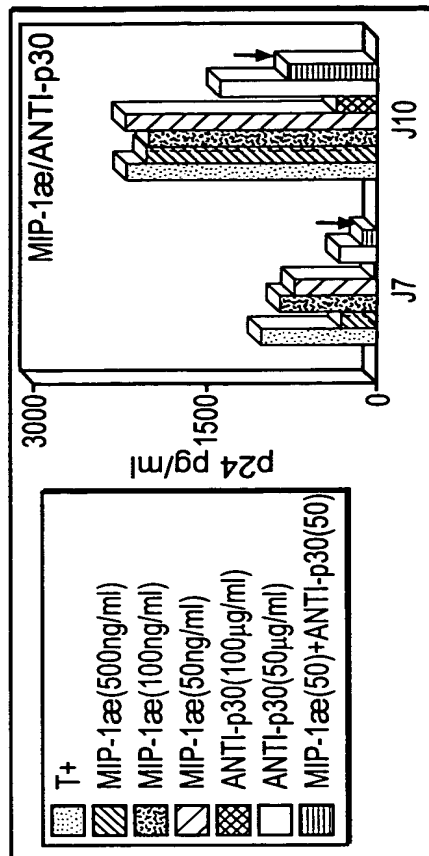
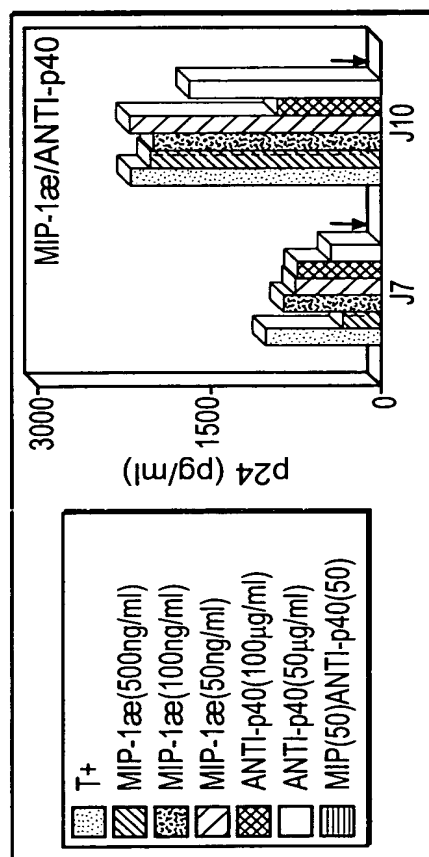


FIG. 46A

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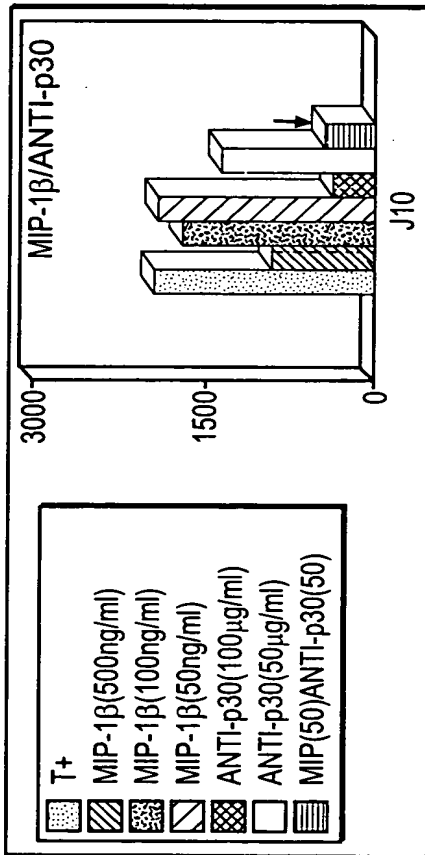
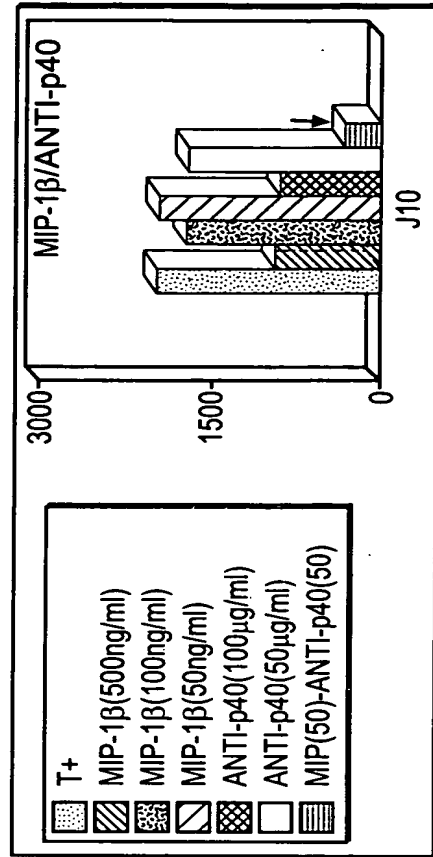


FIG. 46B

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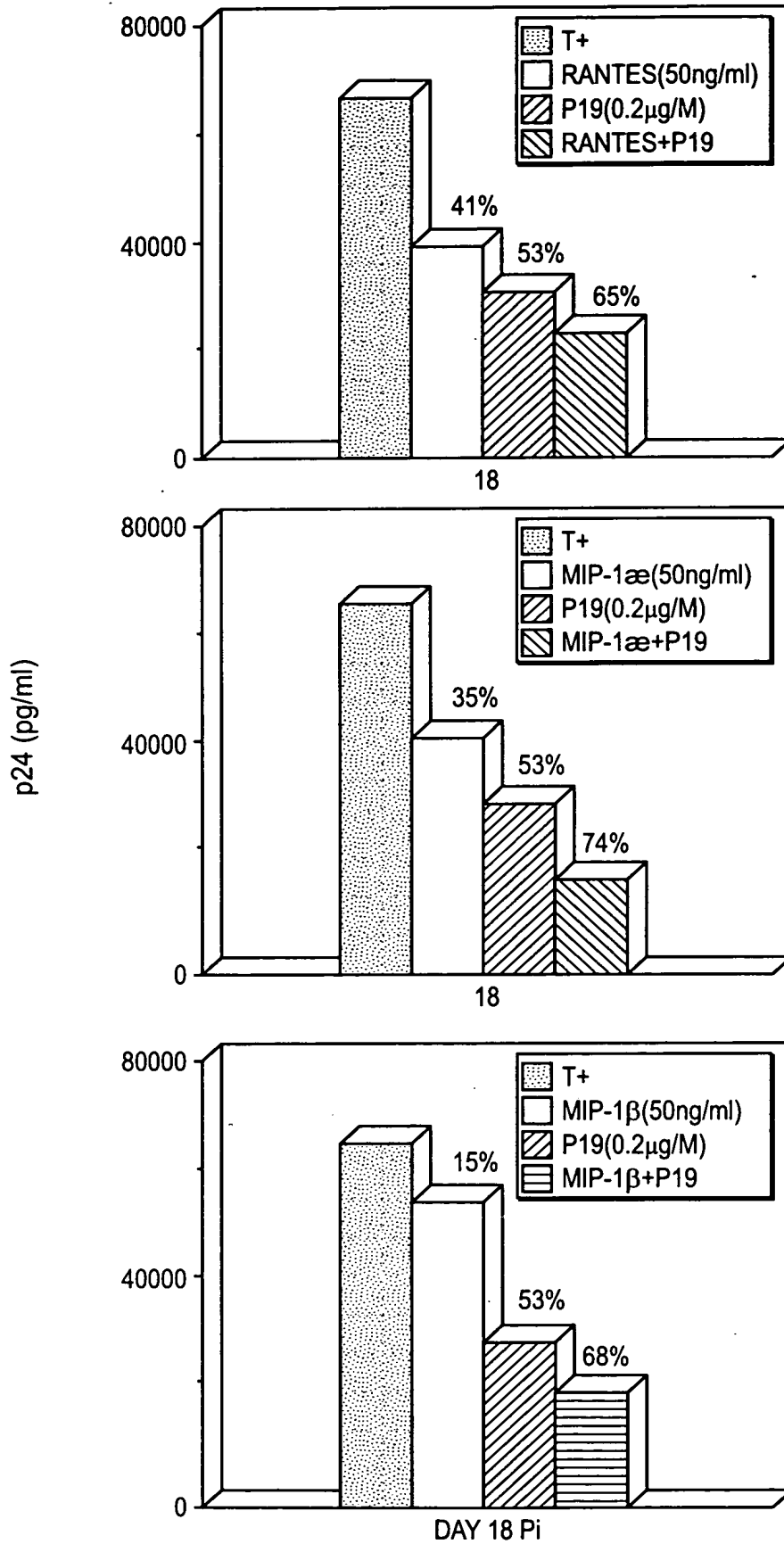


FIG. 47



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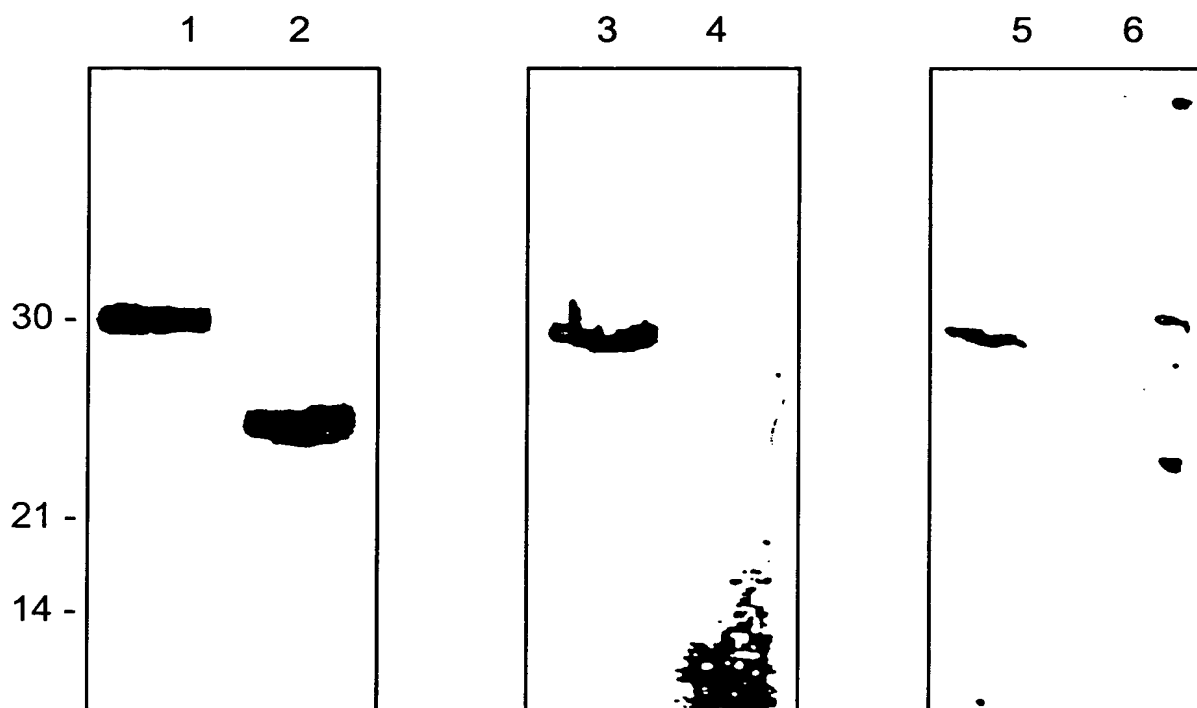


FIG. 48

I. (SEQ ID NO: 22)

```
/translation="MVKLAKAGKNQGDPPKKMAPPPKEVEEDSEDEEMSEDEEDDSSGE  
EVVIPQKKGKAAATSARKVVVSPTKKVAVATPAKKAAPTGGKAAAATPAKKTVTPAK  
AVTTPGKKGATPGKALVATPGKKGAAPAKGAKNGKNAKKEDSDEEEDDDSEDEEDD  
EDEDEDEDEIEPAMKAAAAAPASEDEDDEDDEDDEDDDDDEEDDSEEEAMETTPAKG  
KKAHVVPVKAKNVAEDEDEEEDDEDDEDDDDDEDDEDDEDDDEEEEEEEEEEPVKEA  
PGKRKKEMAKQKAAPEAKKQKVEGTEPTTAFNLFGVGNLNFNSAPELKTGISDVFAKN  
DLAVVDVRIGMTRKFGYVDFESAEDLEKALELTGLKFVGNEIKLEKPKGKDSKKERDA  
RTLLAKNLPYKVTQDELKEVFEDAAEIRLVSKDGKSGIAYIEFKTEADAECTFEKQ  
GTEIDGRSISLYYTGEKGQNQDYRGKNSTWSGESKTLVLNLSYSATEETLQEVFEK  
ATFIKVPQNQNGKSKGYAFIEFASFEDAKEALNSCNKREIEGRAIRLELQGPRGSPNA  
RSQPSKTLFVKGLSEDTTETLKESEFDGSVRARIVTDRETGSSKGFVDFNSEEDAK  
EAMEDGEIDGNKVTLDWAKPKGEGGFGRRGGGRGGFGRRGGGRGGFGRRGRGGFG  
GRGGFRGGRRGGGGDHKPQGGKTKFE"
```

(SEQ ID NO: 23)

II. 1 ATTCTGCTGT AGACATAGAG ATGATGATCA TAGCTGACTA TGATGATGAT
51 CCCCCGCGAG CCTGAAAGAG GAAATGCTCT GGTTCGCTAA GCCCGCGAAT
101 CGAGTGAGAC CCACCCACAA AGCTAACCGT GGAAGTCACT GGC GGCCCTCC
151 TTCGCCCTGC CAGCCGGGGA ACCCATCCGG TGGCTCTCGA CCTGCTCCCG
201 GGCCATCTGG TGACACTGAC TTCGCAGCCA CCACCTTAAT TGGCGCATTC
251 GACCCAAATA ATAACCTGGG AACCTGTGGG CGGTCTAAGG CCCGGCTCTG
301 CGGTCGCCCT CCCAGGCCCC TCTCCCTGGC CCTGTGAGGC CAGAAAGTTA
351 CTTCTCCGAG GCCAGTTCCC CATGTCTGAG AAATATCTCC CAACTTGAGG
401 TTCTGTGGGG TAGGGGAGGG TTCGTGACTT TCTCACAGAA AACCTCGTAC

FIG. 49



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451 AGACCCCGCC ACTGCCTTTA TTAACAGCTC TCAGGAGACT GCCTGCAGGA
501 GGGGGGTCGC TCCGGCCCCA TGCTCGCGGG CAAGCAGGGA TAAGCTGTGC
551 CTCCAAAAGG GCCAACGGGA ACTCCGCGGT CCCTGAACTT CCGGTGCTGG
601 AGGACTCCTC GCTCCAGGGC CACCAGGAGC CGCGGCGTGA GTGCGTGCCG
651 GAACCGAGGG CGGGGTCTCT GAGGAACTCC AAGGCTGCCC AAGCCTACGG
701 ACCCAGCCAC ATTGGCGAAC CGGAGACCGC CCGATTCCAC CACCCCGCG
751 CTCCCCTCAC AGCCGGCGCC AAAAACGCCA GTCCCACGAC GCAGGCCGGG
801 ACCCGCGCGC CCACGGCCCA ATCAGCGCGA CCTTGACAAA AGCGAGCCCC
851 GCCCCACGG CGCCGTTGCC AGCCCCTCCC CCTCCCGTGC CGCCTCGGCC
901 CGCCTACTCC CCGCCCCGCG CCGTTCACGG TTAGAGGCTC GCGATTGGCT
951 CATGGGGACG GCCGCGAGCT TTGGTTGGTC GGCGCGGAGT CACGAGGCGC
1001 CGTCGTCGCC TTTCCACAGG CGTTACTGGG CAGGCTCAGT CTTTCGCCTC
1051 AGTCTCGAGC TCTCGCTGGC TTCGGGTGTA CGTGCTCCGG GATCTTCAGC
1101 ACCCGCGGCC GCCATCGCCG TCGCTTGGCT TCTTCTGGAC TCATCTGCGC
1151 CACTTGTCGG CTTCACTC CGCCGCCATC ATGGTGAAGC TCGCGAAGGT
1201 AAACGGCCTT GAGCGCGACG CAGACGTGTA GGCCTGCTTC CGAGGGGCGA
1251 GCGCGGCGCC GCGGGGAGGA GGCCTGCGC GCAGTCCCGG GCGCGTTCTA
1301 GGGCGCCATG CTGCGGGAAG TCTCGCGCGA TTAGTGGGGA GGTCTCGCGC

FIG. 49 (CONT. 1)



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1351 TTCTGGCTAC TTGGTGGCGA GGTGAAGAGC TTCTGCAGGT GCTGGGGGAG
1401 GGGGCGCTGG GCCTCGGGGT GGAGAGATGA GACCAAACCTT TTGCGACGCG
1451 TACGAGCTGG GACTGACTCT GACGCACGTG CCCGGGAGCG TGCCTGCCAC
1501 GTGGGCCCGC GTAGGTCTGG AATCTCCAGA GGGACCGGGT GCCTTGGGCC
1551 GGGAAATGGC GGTATCGGCC CTAGTCGGAG TCCCGGCTGC GCTCGGATGT
1601 CTCCGCCCCG GCCTGGCAAG CCGATACGTG GTGGGCCCCG GAAGGTGGCT
1651 CTGCCGCGTG CCTTTTGCGC TGTGTTTCGG GCAAGAGGTG GTCCTGCCAG
1701 GTACCCCCAC GTGGCCGCAC CCGCCTCTTT AAGGGGCGGG GTAGTGCTGG
1751 GGAAAGGCAT AAGCTTCATG AGAAAATAAG GTAGTATTTT TAAGTGCCTT
1801 AATGATCTTC ACCGTTAATT TGATTCAAAT AAGGGTGGTA GATAAAGTAC
1851 CGGGATTGTG AGTATAAAAA CACGGTTGTG CTTAACTAAG GTAACGGGAG
1901 GAGAAATCAT TTCCTCAGGT TGACTTTTTA CCTTAGGGCA GGTTTTCTGT
1951 TGGTAAAGCC TGGGAGGAAA AATGTGGGCG GTTGAGAAGT AGTCCCTCTT
2001 GCATTGCCAT CAGGAGTAGT TTCTATGTTA GTTGTGGTGT TTGGCACTAT
2051 GAGAAATGAT CTGAGACGGA GATGATGGCG TATGAACACT AATGGCAAAA
2101 TATGAATGGC CTGAAATGTC GAGGTGGAGG TGTAATGATC TATTTGTGTC
2151 CATTTTAGGC AGGTAAAAAT CAAGGTGACC CCAAGAAAAT GGCTCCTCCT
2201 CCAAAGGAGG TAGAAGAAGA TAGTGAAGAT GAGGAAATGT CAGAAGATGA

FIG. 49 (CONT. 2)



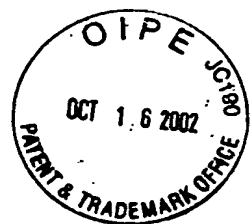
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2251 AGAAGATGAT AGCAGTGGAG AAGAGGTAAT TTTATCCAAC TTAATGCAGA
2301 ATTATGTTAA AACTACAAAA TGGAGAGTTA AGACATGAAA TTGGATATCT
2351 GTGGCAAAAA TAAGATTTTA TCAGGTATGT CTTATTGTAG TGGTTGAGTG
2401 TTTCACAAGC TCTTCATTGA CATGTCAAGA TGTCATTTGG CTAGTATTTG
2451 AATGTGAGTG CTAAGACGAG ACTGGGAATT TCTTTTACAT GTTCCTCTGC
2501 AGGGCTTGGA GTGTGATTTG TTGTGTTAAA TCATTACATT TTTCCAGTTT
2551 CAACATGTTA GCTCACCCCC ACATGTAGAG CTGGGCATTG TATTCAGAGC
2601 TGAGAATAAC CTTACCAGAT TCCTTTCCTA TCCTCCGAAT TAAAATTAAT
2651 TGGTCTCCAT TCCATATATA TATAACTGTA TCACTACTGG TTAAGTACTC
2701 GGGTGTAGAC TGAGGGCTGC CACCTCTCTT TGGTACCATT GACCCTCTTT
2751 AGCCACCTCC TGGCCTTTTA TTTGCCTCCA CTATAAAGAC AGCTGAGCAC
2801 TGAATTGTGC TCAGGTTTTT GTTGAGAACC TGAATGAAAG TTTTACTCTC
2851 CACACATTGC CTTGATAAAA CTACGGGATT TTAATGTAGC TAAATGATGA
2901 CTTTTATCAA ACTACCATGC AACTCTTTG ATGTGTGATA GTTTTGTAAG
2951 GAATATTTAT ATTTAGCCTA TTCATTTTTT GTCTCAGGTC CTAAGAATTG
3001 AGCTTCACTG GGCTTGGTGG ACCGCAACCA CGAGGGCCCC AATGATTTAA
3051 TAAGTTAATG CTTGGAGCCT CCTATGTGTA ACGTTCTGAA TAATTTACAC
3101 ATAGCAATTC ATGACCTTAA ACATGTAAGG ATGATACTAT TACCATTTTC

FIG. 49 (CONT. 3)



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3151 AGATGAGAAA GTTGGGGCTT GGGAAAGTAT GAGGTGTAAG AATTCAGAGG
3201 GTCTGGTTCA GAGGTATTTT CAGTGTTCAA AAGAGTTCCT TATGTCTGGG
3251 TATTCACCTT ATTATAGGGG CTCTGACTTA AGACAACATA ACAGAAGCCT
3301 GGAGTTTTAA CATGTCATAT GTGTCATGCG TATGTCTTGA ACCAGAGGCA
3351 TTGCCAGAGT CTAACAACCTC ATTGGGACCA TGGTTATCTT TTTGGGTGTG
3401 GGGCTGGACT TACTGGTTTG GTTTTCATTT ATCTCAAGGT CGTCATACCT
3451 CAGAAGAAAG GCAAGAAGGC TGCTGCAACC TCAGCAAAGA AGGTGGTCGT
3501 TTCCCCAACA AAAAAGGTTG CAGTTGCCAC ACCAGCCAAG AAAGCAGCTG
3551 TCACTCCAGG CAAAAAGGCA GCAGCAACAC CTGCCAAGAA GACAGTTACA
3601 CCAGCCAAAG CAGTTACCAC ACCTGGCAAG AAGGGAGCCA CACCAGGCAA
3651 AGCATTGGTA GCAACTCCTG GTAAGAAGGG TGCTGCCATC CCAGCCAAGG
3701 GGGCAAAGAA TGGCAAGAAT GCCAAGAAGG AAGACAGTGA TGAAGAGGAG
3751 GATGATGACA GTGAGGAGGA TGAGGAGGAT GACGAGGACG AGGATGAGGA
3801 TGAAGATGAA ATTGAACCAG CAGCGATGAA AGCAGCAGCT GCTGCCCCTG
3851 CCTCAGAGGA TGAGGACGAT GAGGATGACG AAGATGATGA GGATGACGAT
3901 GACGATGAGG AAGATGGTAA GGAGTTGTCT TGGTAGTTAC TGGGCTTCTG
3951 ATTACAAGGT ATCTTGAGAT TCTGGGATCA CATATTCCTT CATCGTACAA
4001 CCTGGAGATG AGATTAGAAT CTTGTGGGAA TTCTCTTGGG TTGTTGTGGT

FIG. 49 (CONT. 4)



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4051 GTGCTAGACT TAATTACCCA TGAATGATTT TGTCCTCTTG AGAAAATTTTC
4101 AATAGCACAT CTATTAGTGT TTTTATAAT GTAGGATTTT CGTTTCTAAG
4151 TGATTTTTTT TTTTTTTTAA ATTTTTTTGA GATGGAGCTT TTGCTGTTTC
4201 CCAGGCGGGA GTGCAATGGC GCGCTATCTC GGCGCACTGC AGCCTCCATC
4251 TCCTGGGTTC AAGCAGTTCT GCCTCAGCCT CCCGAGTAGC GGGATTACAG
4301 GTGCCCACCA CCACACCCTA CTAATTTTGT ATTTTAGTAG AGACGACATT
4351 TCACCATGTT GGCCAGGCTG GCTCTGAACT TTGACCTCAG GTGATCCACC
4401 CACCTTAGGC TCTCCCAAAG TGCTAGGATT ACAGGTGAGA TATGCTGCGC
4451 CCGGCCCCAA GTGATCTATT CTTGCCATGA CTGTAACTA AACATGGTGA
4501 CAGGATTCGA TTTTCTTTAC ATTAGATTTG AAAACCGATG TTGGTTTTGG
4551 GAGATTGCTG CAATTTTTAG GTGACTTCTC TTCAGACTC TGAAGAAGAA
4601 GCTATGGAGA CTACACCAGC CAAAGGAAAG AAAGCTGCAA AAGTTGTTCC
4651 TGTGAAAGCC AAGAACGTGG CTGAGGATGA AGATGAAGAA GAGGATGATG
4701 AGGACGAGGA TGACGACGAC GACGAAGATG ATGAAGATGA TGATGATGAA
4751 GATGATGAGG AGGAGGAAGA AGAGGAGGAG GAAGGTACTT AAATTAGATT
4801 CTGACATACG ACATGAGTTA TGTTTAAAGG AGGCACTTAA GTGTTTGTGG
4851 CTA CTGATGT GTGATACATT GTTTGACATC TTGTCCAGAG CCTGTCAAAG
4901 AAGCACCTGG AAAACGAAAG AAGGAAATGG CCAAACAGAA AGCAGCTCCT

FIG. 49 (CONT. 5)



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4951 GAAGCCAAGA AACAGAAAGT GGAAGGTAAC TTGCAGAATT AGGGGATATG
5001 GGGGAGATAA ACAGCACAAA TGATGAATAA CAAAGGGACT TAATACTGAA
5051 ACCAGATGTT ACATTGTAGT GTGCTGATGT GCTGTGTATA GAAATTTTGC
5101 TTTGGAAACT AACTTTTTAC CACACTACAA GTAGACTGAG TTGAGCTTTT
5151 TTTGTGCAGG CACAGAACCG ACTACGGCTT TCAATCTCTT TGTTGGAAAC
5201 CTAAACTTTA ACAAATCTGC TCCTGAATTA AAAACTGGTA TCAGCGATGT
5251 TTTTGCTAAA AATGATCTTG CTGTTGTGGA TGTCAGAATT GGTATGACTA
5301 GG TAGCTGCT TCACTGCACG TTACATACCG TGGGTCTGTT AATTTTTCCT
5351 TCCCCTGTTA GCACAGTTAC TTTAGCCTGC CACTGT TAAA CATGAATACT
5401 GTAAACACTT CAAGGTTAGC ATTAGTGAAC TAAGTTAGAA TTAAACTGTA
5451 GATCCCCTAA GTTGCAATTT CCATAATCAG TCGTAACTTG GTATAGCACA
5501 GAATAATTTT TAGTAATTTT TTTGTTGTTT TTGTTATGTA TTGAGACGGA
5551 CGCTGGCTTT TGTT CAGGCT GGAGTACAGT GGCGCAATCT TGGCTCACTG
5601 CAACCTCTGC CTCCCGGGTT CAAGCGATTC TCCTGCCTAA CCTCCCAAGT
5651 GACTGGGATA CGGGTGCCAC TCACCATGCA TGGCTAATTT TTGTTTTGTA
5701 TTTAGTATCG ATTT CACCAT GTTGGTCGGC TGGTTTTGAA CTCCTGACCT
5751 CAAGTGATCC ACCCACCTCG GCCTCTCGAA GTGCTGGTAC AGCGTCACCA
5801 CCCTGCCAGT AAGTTTTAAT AATTTGGTGT TAGGTGGGAG AATGCTTGAA

FIG. 49 (CONT. 6)



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5851 CCTGGGAGGC AGAGGTTGCA GTGAGCCAAG TTCGCGCCAC TGTACTCCAG
5901 CCTGGGCAAC AGATTGAGAC ACCGTCTCAA TTAAAATAA TGTTTATTTT
5951 CTTGGAAGTA CCTTGAAACT ATTAGACCTG TCTAGTCATC ATAGTGAATA
6001 CTTTTATCCA GACAGGATTC TCCTGTATTA GTGCTTATAG GTGTTCTTTT
6051 GTCAGCTGCT ACTGTGAATT CTTATAAGCA ATTTAGCTCC ATGATGAAGA
6101 CCTCAAACGT GAATGTGCAT GTCATATCTT CATGCTGAGC CGTGTTCTGT
6151 AGCTGCAGTT TGCAGAGCCT TGACTTTGTT TTGCTATACT AGGGGTGCTT
6201 TTAAAATGT GATCTTTGTT TGCACCATCA CATTTGTCTA GATACAGATT
6251 GTGATTTTGA TTTGTGTTTT CACCTGTTGT AATTTTGCCC TCCTCTCCAC
6301 CTGAAGGAAA TTTGGTTATG TGGATTTTGA ATCTGCTGAA GACCTGGAGA
6351 AAGCGTTGGA ACTCACTGGT TTGAAAGTCT TTGGCAATGA AATTAAACTA
6401 GAGAAACCAA AAGGAAAAGA CAGTAAGAAA GGTATGTAAG GCTTTATGAG
6451 TTATGCAATG AACTCAGGAG CTAGACTGCT AGGGAAAATG CTTTGTAACC
6501 CATTTCCCTT TGGTTTCCTC TTATTTTTTTT TAAATCATTT TTTTCCTTTG
6551 GTTTCCTCTT AATGTGGGAA TTAAATGAGC TACAGTGTTT ACAAGGTACT
6601 TGGCACTGCT TGTCAGTGTA TAGGTAAATT CCTGAGTTAG GCAAGCAAGA
6651 GCACTCTTAT ACAGAACAAG AACCATTACA TGCACCTAAA TTAAGCTAAG
6701 GATCTTTCTT CACTGAAACT AGTTAGGTCC CTAATTACTC CCTATATACA

FIG. 49 (CONT. 7)



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6751 GTGTAATGTT TTGAATTGGT ACATTCACCT TTTTGTGTTAT GCGCGTCTAC
6801 TCTAGGTTGA ACTCCAGTGT ACCTAACAGA GAGTTTGACA TCAAGGCTGT
6851 GACAACATGG AGGGACCACT TGTGTGTTGA CACTGCTATA TCTCCATATT
6901 TAGCACCGAG CCTTGTACAT ATAGGATCTC AAATTATTTG TTGATAGAGC
6951 TATGTGTGTT TTTCCCCTCT TTTTGTGTT GCCCCCCACC TTTGGTTTTT
7001 CAGGCCACAG AGCTCATTTT TGTTTTTTTA ATCTAGAGCG AGATGCGAGA
7051 ACACTTTTGG CTAAAAATCT CCCTTACAAA GTCACCTCAGG ATGAATTGAA
7101 AGAAGTGTTT GAAGATGCTG CGGAGATCAG ATTAGTCAGC AAGGATGGGA
7151 AAAGTAAAGG GTATGTTCTT CTATTGAAAT GTAAGGGTTT TATTAACATT
7201 AATGCACTTC CTGCTTTATA AAAGAAATAT TGGTTTGATT TCCTTAGGCG
7251 TGTAACCTGG ACAGTTTAAC CTGTAAGTTT GTGCCTCAGT AACCCATCTG
7301 TACCATGGGG ATAATGTACT CATAGGGTGA TTTTAAAAGA CAAAGCTAAT
7351 ACTTACAAAG AAGCAAGTTT AATGCCATATC TTACATAAAT ACTTTGTAAG
7401 TAGTAGCAGT TCTTTCAGTG AGGTGAGGTT ACATGAAAAA ATTCCAAGTA
7451 TTTGTAAAAC TAGTGGAAG TAAGAGGGAA GCTCGAGTTT TGATTGAAAA
7501 GTGGACTAAA CAAGGGCATT TTATGTACTC AGATCTGAAG CAAGTTCTGT
7551 GTTGCTGAGG TAAAAGCATT TGTGTTAATA TGGTTTTAAA AACCATGAGT
7601 TCTTCTCCCT CCATTGCAGG ATTGCTTATA TTGAATTTAA GACAGAAGCT

FIG. 49 (CONT. 8)



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7651 GATGCAGAGA AAACCTTTGA AGAAAAGCAG GGAACAGAGA TCGATGGGCG
7701 ATCTATTTCC CTGTACTATA CTGGAGAGAA AGGTCAAAAT CAAGACTATA
7751 GAGGTGGAAA GAATAGCACT TGGAGTGGTA AGAAATTAGG CTTGTTCCAA
7801 GGTTTTTCAGA ATTGGTTGAG GGAACCTCTC TAGTCTTTGT ATTTTCATAAG
7851 TTTATAAATA CTTTTTAATC AAAGTTACTC AAATGTAGGT GAAGATCAAG
7901 GACATGATAC CCCAAGTCAT ACTCTTATTT GGAATAGTAA TTTCCAATCT
7951 TGAAATGAGA GCTCTAAATC ATTTTGCATT GGAATACAGT AGGCAAATCA
8001 AGCTTCCTTT GTAGGCATGT TTTATACTTT AAATGACTTG ACCATGTGCG
8051 TTTTGAAGTC AGATGATTCT AGGAAAACAG ACCAGTCATC AGCCTATGTA
8101 AGAACAACCA GCAGGACATT GCAACACGTA CTAGGTACTT AATATGTTGA
8151 GTAACAGAAA TGGATTTAGC TTACGTCATG AGTATTTGTA TATAACTCAA
8201 GCACTGAAAT TCTTAGGGAA TAGATATTAC TGTTGTGACC GAAGCTGGGA
8251 CACTGTTTCA GAGTCTTAGG AATGTGGCTC TCTATTTCGA GGTGAATCAA
8301 AAACTCTGGT TTTAAGCAAC CTCTCCTACA GTGCAACAGA AGAAACTCTT
8351 CAGGAAGTAT TTGAGAAAGC AACTTTTATC AAAGTACCCC AGAACCAGAA
8401 TGGCAAATCT AAAGGGTAAG ATAATACCTT TGTATCATCA GTTATAGGCC
8451 TATATATGTC TTAGAGGTCT AAGGACGTAA GGTCATGTGT CCTGTAGAAA
8501 AAAGCTAAAT AATTTTAGCC TAGTAAATGA GTGTAAAATA AGTATATTTA

FIG. 49 (CONT. 9)



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8551 GGTCCAACCT TGAGAGAAGG GCCTTGGCCA GATCATGTGA CCAGTGGTAT
8601 AGAGAGCATG TGCCTGGTAA ATTACTCTAA GCATTAAGTGT TTCATCCTCA
8651 GGTATGCATT TATAGAGTTT GCTTCATTCTG AAGACGCTAA AGAAGCTTTA
8701 AATTCCTGTA ATAAAAGGGA AATTGAGGGC AGAGCAATCA GGCTGGAGTT
8751 GCAAGGACCC AGGGGATCAC CTAATGCCAG AAGCCGTAAG TTCACCTGGT
8801 TAGGGTGCTG TGGTTGGGGG TAGCACTCTC GGTGCTTTGT TTATTTTTGC
8851 ACAAATTCTG TGTTTCCTGT TCGCTACTGA GTGAACAATA ACTGGATATC
8901 GATGACTGAT TACCTGAGAA ATAATTGATG AAATCTCAAG AAAATTCCTC
8951 TAGATAGTCA AGTTCTGATC CAGCTGTCTG CAACTCAGAG TAGCAAGTTT
9001 GCCCATGATT TCCTGCCCCA TCCACTGGGC CCCACCTGCT TGGGTTGCTT
9051 TCCCACTTTC CATAGAAGAC TGGGGCAGGA TATCAACTAT GCAATGGCAA
9101 TTAAAAAATG TAAACCCAGA ATAGCCTTTA CTTTAATTAA GGACTAGTTG
9151 GCTTAGTTGC TTTTAACTGC TTTTCACTA TAACAAGTAT CTTGGCTAGT
9201 AGTCATACTA GGCATTGTGC AAATTCAGTG TACGAACTGT GAATTCACAT
9251 AAATCGCAAA TTTTTTTTTT CTTCCCAGAG CCATCCAAAA CTCTGTTTGT
9301 CAAAGGCCTG TCTGAGGATA CCACTGAAGA GACATTAAAG GAGTCATTTG
9351 ACGGCTCCGT TCGGGCAAGG ATAGTTACTG ACCGGGAAAC TGGGTCCTCC
9401 AAAGGGTAAG GGAAGGAAGC GTGAGTGCTG CTTCCACTTG AAGGGGTTTT

FIG. 49 (CONT. 10)



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9451 TGTTCTGTGC AGACCTTGAG TCTAATGTGT CTTCTCATTG AGCTCCTTCT
9501 GTCTATCAGT GGCAGTTTAT GGATTCGCAC GAGAAGAAGA GAGAATTCAC
9551 AGAACTAGCA TTATTTTACC TTCTGTCTTT ACAGAGGTAT ATTTAGCTGT
9601 ATTGTGAGAC ATTCTGGGGT TCAAGCTGTC ACACCAGTTA GTTTTCCATA
9651 GAGAGCTACT CTGCTGCACT GGTATCTTTT TCCCAAATAA ACAAGGCTAC
9701 TTCTGTGGGA TGGCTCCCCA GCATGTACAG TTAAGTTGGG ACATGTGTAG
9751 TAGGTGCTTT TTATAATGGG CAATTTTCATT TGGTGTTCTA GGTTTGGTTT
9801 TGTAGACTTC AACAGTGAGG AGGATGCCAA GGAGGCCATG GAAGACGGTG
9851 AAATTGATGG AAATAAAGTT ACCTTGGACT GGGCCAAACC TAAGGGTGAA
9901 GGTGGCTTCG GGGGTCGTGG TGGAGGCAGA GCGGGCTTTG GAGGACGAGG
9951 TGGTGGTAGA GGAGGCCGAG GAGGATTTGG TGGCAGAGGC CGGGGAGGCT
10001 TTGGAGGTAA GGCACGCAGA GATAATGACA CCACATAGCA TGTGCTCTTC
10051 AGACCCTGTG CCCTGTCACG GTTCCTAATC ACTGGGGAGG AGGAGCTTTG
10101 TACCCATTCT TTAAACAGTG TCTTGCCTTC CTCCTGTAGG GCGAGGAGGC
10151 TTCCGAGGAG GCAGAGGAGG AGGAGGTGAC CACAAGCCAC AAGGAAAGAA
10201 GACGAAGTTT GAATAGCTTC TGTCCCTCTG CTTTCCCTTT TCCATTTGAA
10251 AGAAAGGACT CTGGGGTTTT TACTGTTACC TGATCAATGA CAGAGCCTTC
10301 TGAGGACATT CCAAGACAGT ATACAGTCCT GTGGTCTCCT TGGAAATCCG

FIG. 49 (CONT. 11)



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10351 TCTAGTTAAC ATTTCAAGGG CAATACCGTG TTGGTTTTGA CTGGATATTC
10401 ATATAAACTT TTAAAGAGT TGAGTGATAG AGCTAACCT TATCTGTAAG
10451 TTTTGAATTT ATATTGTTTC ATCCCATGTA CAAAACCATT TTTTCCTACA
10501 AATAGTTTGG GTTTTGTTGT TGTTACTTTT TTTTTTGTTT TTGTTTTTTT
10551 TTTTTTTGCG TTCGTGGGGT TGTAAGAGAA AAGAAAGCAG AATGTTTTAT
10601 CATGGTTTTT GCTTCACCGC TTAGGACAA ATTAAAGTC AACTCTGGTG
10651 CCAGACGTGT TACTTCCTAA AGAGTGTTTC CCCTGGAATC TCACTGGAGA
10701 GCATGGCAAA GCCAGCTCTG CCACTTGCTT CACCCATCCC AATGGAAATG
10751 GCTTAGTGCG TGTTCCAGT ATCCAGCCC TAACTAACTT GGTGAAATG
10801 CTGGTGAGGG GACCTGCTCC TGCAGCCCTG GTGCTGACTT GAAGGCTGCT
10851 GCAGCTTCTC CTACTTTTAG CAGGTCTCGA GGATTATGTC TGAAGACCAC
10901 TCTGGAAGA GGTCGAGGAA CAGATTAGTC AGGTTTCCTA GG

(SEQ ID NO: 24)

III. "MEMGRRIHLELRNRTPSDVKELVLDNSRSNEGKLEGLTDEFEEL
EFLSTINVGLTSIANLPKLNKLELSDNRVSGGLEVLAEKCPNLTHNLSGNKIKD
LSTIEPLKKLENLKSDFNCEVTNLNDYRENVFKLLPQLTYLDGYDRDDKEAPSDA
EGYVEGLDDEEEDEDEEYDEDAQVVEDEDEDEEEEGEEEDVSGEEEDDEEGYNDGE
VDDEEDEEELGEEERGQKRKREPEDEGEDDD"

III. (SEQ ID NO: 25)

1 GCTGGTTGAG CCTTCAAAGT CCTAAAACGC GCGGCCGTGG GTTCGGGGTT

FIG. 49 (CONT. 12)



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51 TATTGATTGA ATTCCGCCGG CGCGGGAGCC TCTGCAGAGA GAGAGCGCGA
101 GAGATGGAGA TGGGCAGACG GATTCATTTA GAGCTGCGGA ACAGGACGCC
151 CTCTGATGTG AAAGAACTTG TCCTGGACAA CAGTCGGTCG AATGAAGGCA
201 AACTCGAAGG CCTCACAGAT GAATTTGAAG AACTGGAATT CTTAAGTACA
251 ATCAACGTAG GCCTCACCTC AATCGCAAAC TTACCAAAGT TAAACAAACT
301 TAAGAAGCTT GAACTAAGCG ATAACAGAGT CTCAGGGGGC CTGGAAGTAT
351 TGGCAGAAAA GTGTCCGAAC CTCACGCATC TAAATTTAAG TGGCAACAAA
401 ATTAAAGACC TCAGCACAAT AGAGCCACTG AAAAAGTTAG AAAACCTCAA
451 GAGCTTAGAC CTTTTCAATT GCGAGGTAAC CAACCTGAAC GACTACCGAG
501 AAAATGTGTT CAAGCTCCTC CCGCAACTCA CATATCTCGA CGGCTATGAC
551 CGGGACGACA AGGAGGCCCC TGA CTGAGGGCT ACGTGGAGGG
601 CCTGGATGAT GAGGAGGAGG ATGAGGATGA GGAGGAGTAT GATGAAGATG
651 CTCAGGTAGT GGAAGACGAG GAGGACGAGG ATGAGGAGGA GGAAGGTGAA
701 GAGGAGGACG TGAGTGGAGA GGAGGAGGAG GATGAAGAAG GTTATAACGA
751 TGGAGAGGTA GATGACGAGG AAGATGAAGA AGAGCTTGGT GAAGAAGAAA
801 GGGGTCAGAA GCGAAAACGA GAACCTGAAG ATGAGGGAGA AGATGATGAC
851 TAAGTGAAT AACCTATTTT GAAAATTCC TATTGTGATT TGA CTGTTTT
901 TACCCATATC CCCTCT

FIG. 49 (CONT. 13)



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IV. (SEQ ID NO: 26)

"MSAPAAKVSKKELNSNHDGADETSEKEQQEAIEHIDEVQNEIDR
LNEQASEEILKVEQKYNKLRQPFQKRSELIAKIPNFWTTFVNHQPVSALLGEEDEE
ALHYLTRVEVTEFEDIKSGYRIDFYFDENPYFENKVLSEFHLNESGDPSSKSTEIKW
KSGKDLTKRSSQTQNKASRKQHEEPESFFTWFTDHS DAGADELGEVIKDDIWPNPLO
YYLVPDMDDEEGEGEEDDDDEEEGLEIDEEGDEDEGEDEEDDDDEGEEGEEDGED
D"

IV. (SEQ ID NO: 27)

1 CGACCGCGGA GCAGCACCAT GTCGGCGCCG GCGGCCAAAG TCAGTAAAAA
51 GGAGCTCAAC TCCAACCACG ACGGGGCCGA CGAGACCTCA GAAAAAGAAC
101 AGCAAGAAGC GATTGAACAC ATTGATGAAG TACAAAATGA AATAGACAGA
151 CTTAATGAAC AAGCCAGTGA GGAGATTTTG AAAGTAGAAC AGAAATATAA
201 CAAACTCCGC CAACCATTTT TTCAGAAGAG GTCAGAATTG ATCGCCAAAA
251 TCCCAAATTT TTGGGTAACA ACATTTGTCA ACCATCCACA AGTGTCTGCA
301 CTGCTTGGGG AGGAAGATGA AGAGGCACTG CATTATTTGA CCAGAGTTGA
351 AGTGACAGAA TTTGAAGATA TTAAATCAGG TTACAGAATA GATTTTTATT
401 TTGATGAAAA TCCTTACTTT GAAAATAAAG TTCTCTCCAA AGAATTTTCAT
451 CTGAATGAGA GTGGTGATCC ATCTTCGAAG TCCACCGAAA TCAAATGGAA
501 ATCTGGAAAG GATTTGACGA AACGTTGAG TCAAACGCAG AATAAGCCA
551 GCAGGAAGAG GCAGCATGAG GAACCAGAGA GCTTCTTTAC CTGGTTTACT
601 GACCATTCTG ATGCAGGTGC TGATGAGTTA GGAGAGGTCA TCAAAGATGA

FIG. 49 (CONT. 14)



651 TATTGGCCA AACCCATTAC AGTACTACTT GGTCCCGAT ATGGATGATG
701 AAGAAGGAGA AGGAGAAGAA GATGATGATG ATGATGAAGA GGAGGAAGGA
751 TTAGAAGATA TTGACGAAGA AGGGGATGAG GATGAAGGTG AAGAAGATGA
801 AGATGATGAT GAAGGGGAGG AAGGAGAGGA GGATGAAGGA GAAGATGACT
851 AAATAGAACA CTGATGGATT CCAACCTTCC TTTTTTTAAA TTTTCTCCAG
901 TCCCTGGGAG CAAGTTGCAG TCCT

V. (SEQ ID NO: 28)

CTTCGGGTGTACGTGCTCCGGGATCTTCAGCACCCGGGGCCCATCGCCGTCGCTTGGCTTCTTGGACTCATCTGCCG
CCACTTGTCCGCTTCACACTCCGGCGCCATCATGTGTGAAGCTCGCGAAGGCAGGTAAAAATCAAGGTGACCCCAAGAAAA
TGGCTCCTCCTCCAAAGGAGGTAGAAGAAGATAGTGAAGATGAGGAAATGTGAGAAGATGAAGAAGATGATAGCAGTGA
GAAGAGGTGCTCATACCTCAGAAGAAAGGCAAGAGGCTGTGCAACCTCAGCAAAGAGGTGGTGGTTCCTCCCAACAAA
AAAGGTTGCAGTTGCCACACAGCCAAAGAAAGCAGCTGTCACTCCAGGCAAAAGGCAGCAGCAACACCTGCCAAGAAGA
CAGTTACACGACCAAGCAGTTACCAACCTGGCAAGAGGGAGCCACACAGGCAAAAGCATTTGGTAGCAACTCCTGGT
AAGAAGGTGCTGCCATCCAGCAAGGGGCAAGAATGGCAAGAATGCCAAGAAGGACACAGTATGAAGAGGAGGA
TGATGACAGTGAGGAGGATGAGGAGGATGACGAGGACGAGGATGAGGATGAAGATGAATGAATGAACCGAGCGGATGAAG

FIG. 49 (CONT. 15)



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CAGCAGCTGCTGCCCTCAGAGGATGAGGACGATGAGGATGACGAAGATGATGAGGATGACGATGACGATGAGGAA
GATGACTCTGAAGAAGAGCTATGGAGACTACACCGCCAAAGGAAAGCTGCAAAAGTTGTTCTCTGTGAAAGCCAA
GAACGTGGCTGAGGATGAAGATGAAGAAGAGGATGATGAGGACGAGGATGACGACGACGAGGATGATGAAGATGATG
ATGATGAAGATGATGAGGAGGAGGAAGAAGAGGAGGAGGAAGAGCCTGTCAAAGAACACCTTGGAACCGAAGAGGAA
ATGGCCAAACAGAAAGCAGCTCCTGAAGCCAAAGAAACAGAAAGTGGAAGGCACAGAACCGACTACGGCTTCAATCTCTT
TGTGGAAACCTAAACTTTAACAAATCTGCTCCTGAATTAATAACTGGTATCAGGATGTTTTCCTTAAATAATGATCTTG
CTGTTGTGATGTCAGAAATTGGTATGACTAGGAAATTTGGTTATGTGGATTTTGAATCTGCTGAGACCTGGAGAAAGCG
TTTGGAACTCACTGGTTTGAAGCTCTTTGGCAATGAAATTAACCTAGAGAAACCCAAAGGAAAGACAGTAAAGAGAGCG
AGATCGGAGAACACTTTTGGCTAAAAATCTCCCTTACAAAGTCACTCAGGATGAAATTGAAAGAGTGTGGAAGATGCTG
CGGAGATCAGATTAGTCAGCAAGGATGGGAAAGTAAAGGATTCCTTATATTAATTAAGACAGAGCTGATGCGAGAG
AAAACTTTGAAGAAAGCAGGGAACAGAGATCGATGGCGGATCTATTTCCCTGTACTATCTGAGAGAAAGGTCAAAA
TCAAGACTATAGAGGTGGAAGAAATAGCACTTGGAGTGGTGAATCAAAAACCTCTGGTTTAAAGCAACCTCTCCTACAGTG
CAACAGAAGAAACTCTTCAGGAAGTATTTGAGAAAGCAACTTTTATCAAAGTACCCAGAACCCAAATGGCAAAATCTAAA
GGGTATGCATTTATAGAGTTTCTTCAATTCGAAGACGCTAAAGAGCTTTAAATTCCTGTAAATAAAGGAAATTTGAGGG
CAGAGCAATCAGGCTGGAGTTGCAAGGACCCAGGGGATCACCTAATGCCAGAAGCCAGCCATCCAAAACCTCTGTTTGCA
AAGCCCTGCTGAGGATACCACTGAAGAGACATTAAGGAGTCAATTTGACGGCTCCGTTCCGGCAAGGATAGTTACTGAC
CGGAAACTGGGTCTCCAAAGGTTTGGTTTGTAGACTTCAACAGTGAAGGATGCCAAGGAGGCCATGGAAGACGG
TGAAATGATGGAATAAAGTTACCTTGGACTGGGCCAAACCTAAGGTGAAGTGGCTTCGGGGGTCTGTTGGAGGCA
GAGCCGGCTTTGGAGGACGAGGTGGTGTAGAGAGGCCGAGGAGGATTTGGTGGCAGAGGCCGGGAGGCTTTGGAGGG
CGAGGAGGCTTCCGAGGCGCAGAGGAGGAGGTGACCAACAGCCACAGGAAGAAAGACGAAAGTTGAATAGCTTCT
GTCCCTCTGCTTTTCCCTTTTCCATTTGAAAGAAAGGACTCTGGGGTTTTTACTGTACCTGATCAATGACAGAGCCTTCT
GAGGACATTTCCAAGACAGTATACAGTCTCTGTTGCTCTCTTGGAAATCCGCTCTAGTTAACATTTCAAGGGCAATACCGTGT
TGGTTTGTGACTGGATATTCATATAAACTTTTAAAGAGTTGAGTGATAGAGCTAACCTTATCTGTAAGTTTGAATTTA
TATTGTTTCATCCCATGTACAAAACCATTTTTTCCCTAC

FIG. 49 (CONT. 16)